GenCore version 5.1.6
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SW protein - protein search, using sw model

Run on: June 14, 2004, 15:07:46 ; Search time 17.3654 Seconds
(without alignments)
224.455 Million cell updates/sec

Title: US-09-249-011B-8
Perfect score: 681
Sequence: 1 MDSQAQVLIIIILLWVSGTCG.....YCIQSYNEYIFPGQGIKVEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	592	86.9	239	1	US-08-453-400-37	Sequence 37, Appl
2	553.5	81.3	135	3	US-08-812-590-46	Sequence 46, Appl
3	548.5	80.5	133	3	US-08-463-903-4	Sequence 4, Appli
4	548.5	80.5	133	4	US-07-935-695-4	Sequence 4, Appli
5	548	80.5	241	2	US-07-916-098A-56	Sequence 56, Appl
6	547.5	80.4	240	4	US-09-301-593-36	Sequence 36, Appl
7	528.5	77.6	133	2	US-08-822-028-12	Sequence 12, Appl
8	528.5	77.6	133	4	US-08-479-285-12	Sequence 12, Appl
9	526.5	77.3	133	5	PCT-US93-11611-2	Sequence 2, Appli
10	525.5	77.2	133	4	US-09-301-593-24	Sequence 24, Appl
11	525.5	77.2	240	4	US-09-301-593-28	Sequence 28, Appl
12	522.5	76.7	154	3	US-08-513-968-36	Sequence 36, Appl
13	513.5	75.4	495	3	US-08-828-741B-4	Sequence 4, Appli
14	513.5	75.4	495	4	US-09-160-567-4	Sequence 4, Appli
15	512.5	75.3	133	4	US-08-579-478A-2	Sequence 2, Appli
16	512.5	75.3	133	5	PCT-US93-11612-2	Sequence 2, Appli
17	504.5	74.1	113	4	US-09-301-593-6	Sequence 6, Appli
18	504.5	74.1	113	4	US-09-301-593-34	Sequence 34, Appl
19	502.5	73.8	113	4	US-08-526-539A-80	Sequence 80, Appl
20	502.5	73.8	155	3	US-08-828-741B-11	Sequence 11, Appl
21	502.5	73.8	155	4	US-09-160-567-11	Sequence 11, Appl
22	502.5	73.8	342	3	US-08-828-741B-6	Sequence 6, Appli
23	502.5	73.8	342	4	US-09-160-567-6	Sequence 6, Appli
24	500.5	73.5	113	4	US-09-301-593-2	Sequence 2, Appli
25	500.5	73.5	113	4	US-09-301-593-32	Sequence 32, Appl
26	500.5	73.5	114	4	US-09-025-769B-17	Sequence 17, Appl
27	498.5	73.2	113	5	PCT-US93-08435-8	Sequence 8, Appli
28	498.5	73.2	275	3	US-08-463-903-6	Sequence 6, Appli
29	498.5	73.2	275	4	US-07-935-695-6	Sequence 6, Appli
30	497.5	73.1	115	4	US-09-025-769B-31	Sequence 31, Appl
31	497.5	73.1	115	4	US-09-025-769B-49	Sequence 49, Appl
32	496.5	72.9	114	1	US-08-336-125-6	Sequence 6, Appli
33	496.5	72.9	114	2	US-08-459-578-6	Sequence 6, Appli
34	496.5	72.9	114	2	US-09-017-628-6	Sequence 6, Appli
35	496.5	72.9	114	2	US-09-014-080-6	Sequence 6, Appli
36	496.5	72.9	114	4	US-08-450-464-6	Sequence 6, Appli
37	496	72.8	112	1	US-07-942-245-30	Sequence 30, Appl
38	494.5	72.6	171	3	US-08-463-903-20	Sequence 20, Appl
39	494.5	72.6	171	4	US-07-935-695-20	Sequence 20, Appl
40	494	72.5	114	4	US-08-929-856-66	Sequence 66, Appl
41	491.5	72.2	133	5	PCT-US93-11611-9	Sequence 9, Appli
42	490.5	72.0	113	5	PCT-US93-08435-6	Sequence 6, Appli
43	490	72.0	219	1	US-08-453-400-34	Sequence 34, Appl
44	489.5	71.9	265	3	US-08-463-903-22	Sequence 22, Appl
45	489.5	71.9	265	4	US-07-935-695-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-453-400-37
; Sequence 37, Application US/08453400
; Patent No. 5665857
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-453-400-37

Query Match 86.9%; Score 592; DB 1; Length 239;
Best Local Similarity 84.8%; Pred. No. 4.2e-48;
Matches 112; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MDSQAQVLIIIILLWVSGTCGSFTSLAVSLSERATLSCRASQSLLNSKTKENFLA 56
|||||:|||||||||:|||||||:||| ||||| || :|||||||||||||:|||
Db 1 MDSQAPVLIIIILLWVSGIDGSFTSLAVSLSERVTMSCRSSQSLLNSKTKENYLA 56

Qy 57 WYQQKPGQAPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSVQAEDLAIYYCKQSYN 116
|||:|||:|||||||||||||:|||||||||||||||||||||||||||||||||||
Db 57 WYQQRPGQSPKLLIYWASIRESGVPDRFSGSGSGTDFTLTISSVQAEDLAIYYCKQSYN 116

Qy 117 EYIFPGQGIKVEIK 132
||| |||||||||
Db 117 EYIFPGQGIKLEIK 132

RESULT 2

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US-08-812-586-46
; Sequence 46, Application US/08812586
; Patent No. 6048704
;  GENERAL INFORMATION:
;    APPLICANT:  Martin David Tilson
;    TITLE OF INVENTION:  PURIFIED AND RECOMBINANT ANTIGENIC
;    TITLE OF INVENTION:  PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYM (AAA)
;    TITLE OF INVENTION:  DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/812,586
;      FILING DATE:  07-MAR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  [illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  135 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-812-586-46

  Query Match             81.4%;  Score 548.5;  DB 4;  Length 135;
  Best Local Similarity   84.6%;  Pred. No. 1e-44;
  Matches  110;  Conservative    6;  Mismatches   14;  Indels    1;  Gaps    1;

Qy           4 QAQVTLKESGPALVKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIYWDDDKRYNPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCARIRPAYGNYVMDYWGQGTLVTVSS 123
             | |||| |||||||  |||||||||||||||||||||||||||||||||||||| |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLLYYYYGMDVWGQGTTVTVSS 123

Qy         124 PGQGIKVEIK 133
               |||||||||| |
Db         124 PGQGIKVVIK 133


RESULT 4
US-08-463-603-4
;  NUMBER OF SEQ ID NOS:  102
;  SOFTWARE:  MS-Word for Windows, Ver. 7.0
; SEQ ID NO 4
;    LENGTH:  133
;    TYPE:  PRT
;    ORGANISM:  Homo sapiens
;    FEATURE:
;    NAME/KEY:  Human Kappa subgroup IV VL (Hum4 VL) from pKL1001
;    LOCATION:  1..133
US-08-463-603-4

  Query Match             80.5%;  Score 548.5;  DB 4;  Length 133;
  Best Local Similarity   83.8%;  Pred. No. 2.9e-44;
  Matches  109;  Conservative    6;  Mismatches   14;  Indels    1;  Gaps    1;

Qy           4 QAQVTLKESGPALVKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIYWDDDKRYNPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCARIRPAYGNYVMDYWGQGTLVTVSS 123
             | |||| |||||||  |||||||||||||||||||||||||||||||||||||| |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLLYYYYGMDVWGQGTTVTVSS 123

Qy         124 PGQGIKVEIK 133
               |||||||||| |
Db         124 PGQGIKVVIK 133


RESULT 4
US-07-935-695-4
; Sequence 4, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Richard, Ruth A.
;  APPLICANT:  Altholter, Joseph A.
;  APPLICANT:  Kotite, Nicolas J.
;  TITLE OF INVENTION:  Dimer and Multimer Forms of Single Chain Polypeptides
;  FILE REFERENCE:  40221A-US
;  CURRENT APPLICATION NUMBER:  US/07/935,695
;  CURRENT FILING DATE:  1992-08-21
;  PRIOR APPLICATION NUMBER:  US 08/463,603
;  PRIOR FILING DATE:  1995-06-05
;  NUMBER OF SEQ ID NOS:  102
;  SOFTWARE:  MS-Word for Windows, Ver. 7.0
; SEQ ID NO 4
;    LENGTH:  133
;    TYPE:  PRT
;    ORGANISM:  Homo sapiens
;    FEATURE:
;    NAME/KEY:  Human Kappa subgroup IV VL (Hum4 VL) from pKL1001
;    LOCATION:  1..133
US-07-935-695-4

  Query Match             80.5%;  Score 548.5;  DB 4;  Length 133;
  Best Local Similarity   83.8%;  Pred. No. 2.9e-44;
  Matches  109;  Conservative    6;  Mismatches   14;  Indels    1;  Gaps    1;

Qy           4 QAQVTLKESGPALVKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIYWDDDKRYNPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCARIRPAYGNYVMDYWGQGTLVTVSS 123
             | |||| |||||||  |||||||||||||||||||||||||||||||||||||| |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLLYYYYGMDVWGQGTTVTVSS 123

Qy         124 PGQGIKVEIK 133
               |||||||||| |
Db         124 PGQGIKVVIK 133


RESULT 5
US-07-916-898A-56
```

; Sequence 55, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BOEKLY, LINDA F.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09412
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/619,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715 1244
; TELEX: 910/221-5417
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-916-098A-56

Query Match 80.5%; Score 548; DB 2; Length 241;
Best Local Similarity 83.6%; Pred. No. 5.3e-44;
Matches 107; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 5 AQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLAWYQQ 64
||:|:|||||:|:|||||||||||||||||||||||||||||||||||||||||||||||||
Db 7 AQLLCLLLLWLPGARCEIVMTQSPGTLSLAVSPGERATINCKSSQSLLNSRTRKNYLAWYQQ 66

Qy 65 KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNLYTFG 124
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 67 KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNLYTFG 126

Qy 125 QGTKVEIK 132
||||||||
Db 127 QGTKLEIK 134

RESULT 6
US-09-301-593A-36
; Sequence 36, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Grijalva-Chosa, Pilar
; APPLICANT: Rambotepe, Uwe
; APPLICANT: Lester, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Bottig, Wolfgang J.
; TITLE OF INVENTION: FAT specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.189000
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593A-36

Query Match 80.4%; Score 542.5; DB 4; Length 240;
Best Local Similarity 82.1%; Pred. No. 7e-44;
Matches 110; Conservative 10; Mismatches 11; Indels 3; Gaps 2;

Qy 1 MEST[illegible]WVSGTCGDIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRENYLA 60
|:: :| :|||| |: ||||:|||||||||||||||||||:|||| || || :|||:|
Db 1 MGIKMESQTQVFVFVFLLCLSGVDGDIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLA 60

Qy 61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNLY 120
|||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||| | |
Db 61 WYQEKPGLAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP 120

Qy 121 TFGQGTKVEIK 132
|||||||||||
Db 121 PLTFGGGTKVEIK 133

RESULT 7
US-08-822-028-12
; Sequence 12, Application US/08822028
; Patent No. 5993813
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCRIBNER, JEFFERY
; TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
; TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUANE C ULMER
; STREET: P.O. BOX 1967
; CITY: MIDLAND
; STATE: MICHIGAN
; COUNTRY: USA
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,028
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/040,667
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C

```
      REGISTRATION NUMBER:  34,941
      REFERENCE/DOCKET NUMBER:  C 37,075C
    TELECOMMUNICATION INFORMATION:
      TELEPHONE:  (517) 636 8104
  INFORMATION FOR SEQ ID NO:  12:
    SEQUENCE CHARACTERISTICS:
      LENGTH:  133 amino acids
      TYPE:  amino acid
      TOPOLOGY:  linear
    MOLECULE TYPE:  protein
US-08-822-028-12

  Query Match             77.6%;  Score 528.5;  DB 2;  Length 133;
  Best Local Similarity   75.9%;  Pred. No. 2.2e-42;
  Matches  101;  Conservative   16;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 MDSQAQVLLLLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRKNYLA 60
              ||||||||:|||||||||||||||||:|:| || |||||: |:|||||||| | ::|||||
Db          1 MDSQAQVLMLLLLWVSGTCGDIVMSQSPDSLPVSVGEKVTISCKSSQSLLYSSNQKNYLA 60

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNL 120
              |||||||| |||||||| |||||||||:|||||||||:|:|||:: ||:|||||| | |:
Db         61 WYQQKPGQSPKLLIYWASARESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSY 120

Qy        121  YTFGQGTKVEIK 132
                 ||| ||| :|
Db        121 FTFGAGTKLVLK 132


RESULT 8
US-08-479-285-12
; Sequence 12, Application US/08479285
; Patent No. 5620615
; GENERAL INFORMATION:
;     APPLICANT:  MEZES, PETER S
;     APPLICANT:  GOURLIE, BRIAN B
;     APPLICANT:  KIXON, MARK W
;     APPLICANT:  ANDERSON, WH KERR
;     APPLICANT:  KAPLAN, DONALD A
;     APPLICANT:  SCHOLOM, JEFFREY
;     TITLE OF INVENTION:  A NOVEL FAMILY OF HIGH AFFINITY,
;     TITLE OF INVENTION:  MODIFIED ANTIBODIES FOR CANCER TREATMENT
;     NUMBER OF SEQUENCES:  74
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  DUANE C OLMER
;       STREET:  P.O. BOX 1967
;       CITY:  MIDLAND
;       STATE:  MICHIGAN
;       COUNTRY:  USA
;       ZIP:  48641 1967
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC DOS/MS DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/479,285
;       FILING DATE:  07 JUN 1995
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/043687
;       FILING DATE:  31 MAR 1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  OLMER, DUANE C
;       REGISTRATION NUMBER:  34,941
;       REFERENCE/DOCKET NUMBER:  C 37,075C
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (517) 636 8104
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  133 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-479-285-12

  Query Match             77.6%;  Score 528.5;  DB 4;  Length 133;
  Best Local Similarity   75.9%;  Pred. No. 2.2e-42;
  Matches  101;  Conservative   16;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 MDSQAQVLLLLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRKNYLA 60
              ||||||||:|||||||||||||||||:|:| || |||||: |:|||||||| | ::|||||
Db          1 MDSQAQVLMLLLLWVSGTCGDIVMSQSPDSLPVSVGEKVTISCKSSQSLLYSSNQKNYLA 60

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNL 120
              |||||||| |||||||| |||||||||:|||||||||:|:|||:: ||:|||||| | |:
Db         61 WYQQKPGQSPKLLIYWASARESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSY 120

Qy        121  YTFGQGTKVEIK 132
                 ||| ||| :|
Db        121 FTFGAGTKLVLK 132


RESULT 9
PCT-US93-11611-2
; Sequence 2, Application US/08479285
; GENERAL INFORMATION:
;     APPLICANT:  Co, Man Sung
;     APPLICANT:  Landolfi, Nicholas F.
;     TITLE OF INVENTION:  Humanized Antibodies Reactive with CD18
;     NUMBER OF SEQUENCES:  11
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend Khourie and Crew
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/11611
;       FILING DATE:  30 NOV 1993
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/983,949
;       FILING DATE:  01 DEC 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William M.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  11824 45
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326 2400
;       TELEFAX:  415 326-2422
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  133 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US93-11611-2

  Query Match             72.4%;  Score 526.5;  DB 5;  Length 133;
  Best Local Similarity   76.7%;  Pred. No. 3.3e-42;
  Matches  102;  Conservative   16;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          1 MDSQAQVLLLLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRKNYLA 60
              |||||:|||||||||||||||||:|:| || |||||: |:|||||||| | ::|||||
Db          1 MDSQAQVLMLLLLWVSGTCGDIVMSQSPDSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLA 60

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNL 120
              |||||||| |||||||||||||||||:|||||||||:|:|||:: ||:|||||| | |:
Db         61 WYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSY 120
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Qy          121  YIFGQGIKVEIK 132
                 :|||| |||:|||
Db          121 PFIFGSGIKLEIK 133


RESULT 10
US-09-301-593-24
; Sequence 24, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
;  APPLICANT: Park, John E.
;  APPLICANT: Garin-Chesa, Pilar
;  APPLICANT: Bamberger, Uwe
;  APPLICANT: Leger, Olivier
;  APPLICANT: Saldanha, Jose W.
;  APPLICANT: Rettig, Wolfgang J.
;  TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
;  FILE REFERENCE: 0652.1890001
;  CURRENT APPLICATION NUMBER: US/09/301,593A
;  CURRENT FILING DATE: 1999-04-29
;  EARLIER APPLICATION NUMBER: EP 98107925.4
;  EARLIER FILING DATE: 1998-04-30
;  EARLIER APPLICATION NUMBER: US 60/086,049
;  EARLIER FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 133
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-301-593-24

  Query Match             77.2%;  Score 525.5;  DB 4;  Length 133;
  Best Local Similarity   77.6%;  Pred. No. 4.1e-42;
  Matches  104;  Conservative   15;  Mismatches   12;  Indels    3;  Gaps    2;

Qy           1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLA 60
               |||||||||:|| |||||||||||:||| |||||:|| |:|||||||| || ::|||
Db           1 MDSQAQVLMLLFLWVSGICGEIVMSQSPDSLAVSVGEKVTMSCKSSQSLLYSRNQKNYLA 60

Qy          61 WYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQ -SY 118
               :|||||| |||||:|||||||||||||:||| |||| |||||:|||:||| | |  ||
Db          61 WFQQKPGQSPKLLIFWASTRESGVPDRFTGSGSGTDFNLTISSVQAEDLAVYYCQQYFSY 120

Qy         119 NLYTFGQGIKVEIK 132
                 | ||| |||:|
Db         121 PLTFGAGTKLELK 133


RESULT 11
US-09-301-593-28
; Sequence 28, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
;  APPLICANT: Park, John E.
;  APPLICANT: Garin-Chesa, Pilar
;  APPLICANT: Bamberger, Uwe
;  APPLICANT: Leger, Olivier
;  APPLICANT: Saldanha, Jose W.
;  APPLICANT: Rettig, Wolfgang J.
;  TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
;  FILE REFERENCE: 0652.1890001
;  CURRENT APPLICATION NUMBER: US/09/301,593A
;  CURRENT FILING DATE: 1999-04-29
;  EARLIER APPLICATION NUMBER: EP 98107925.4
;  EARLIER FILING DATE: 1998-04-30
;  EARLIER APPLICATION NUMBER: US 60/086,049
;  EARLIER FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-301-593-28

  Query Match             77.2%;  Score 525.5;  DB 4;  Length 240;
  Best Local Similarity   77.6%;  Pred. No. 7.7e-42;
  Matches  104;  Conservative   15;  Mismatches   12;  Indels    3;  Gaps    2;

Qy           1 M[illegible]:|||||||||:|| |||||||||||:||| |||||:|| |:|||||||| || ::|||
Db           1 MDSQAQVLMLLFLWVSGICGDIVMSQSPDSLAVSVGEKVTMSCKSSQSLLYSRNQKNYLA 60

Qy          61 WYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQ -SY 118
               :|||||| |||||:|||||||||||||:||| |||| |||||:|||:||| | |  ||
Db          61 WFQQKPGQSPKLLIFWASTRESGVPDRFTGSGSGTDFNLTISSVQAEDLAVYYCQQYFSY 120

Qy         119 NLYTFGQGIKVEIK 132
                 | ||| |||:|
Db         121 PLTFGAGTKLELK 133


RESULT 12
US-08-513-968-36
; Sequence 36, Application US/08513968
; Patent No. 6114143
;  GENERAL INFORMATION:
;    APPLICANT:  EDA, Yasuyuki
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  MAKIZUMI, Koichi
;    APPLICANT:  SHIOSAKI, Koichi
;    APPLICANT:  OSATOMI, Kiyoshi
;    APPLICANT:  KIMACHI, Kazuhiko
;    APPLICANT:  HIGUCHI, Hirofumi
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  ANTI HIV MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,968
;      FILING DATE:  11-SEP-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7091/1993
;      FILING DATE:  13-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  EDA 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  154 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  linear
;    MOLECULE TYPE:  protein
US-08-513-968-36

  Query Match             26.7%;  Score 522.5;  DB 5;  Length 154;
  Best Local Similarity   25.2%;  Pred. No. 9.1e-42;
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  Matches  130;  Conservative    14;  Mismatches   18;  Indels     1;  Gaps     1;

Qy           1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLA 60
               |||  ||  || |||||||||||:|||| || |:|:|| |||||||||||||  :|||
Db           5 MESQTLVFVSMSLLWVSGVYGEIVMSQSPDFQSVTPKEKVTITCRASQSIGSNIHWYQQK 64

Qy          61 WYQQKPDQSPKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
               |||||||||||||||||| |||||||:|||| |||||||||:|||||||||||||||   |:
Db          65 WYQQKPDQSPKFLIYWASTGESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSY 124

Qy         121  YTFGQGTKVEIK 132
                :|||  |||:|||
Db         125 FWFGGGTKLEIK 136


RESULT 13
US-08-828-741B-4
; Sequence 4, Application US/08828741B
; Patent No. 6044069
;  GENERAL INFORMATION:
;     APPLICANT:  Koenigsen, Frank
;     APPLICANT:  Suess, Gabriele M.
;     APPLICANT:  Farlinton, David M.
;     APPLICANT:  Freutlein, Herbert R.
;     TITLE OF INVENTION:  CATALYTIC ANTIBODIES AND A METHOD OF
;     TITLE OF INVENTION:  PRODUCING SAME
;     NUMBER OF SEQUENCES:  14
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;       STREET:  400 Garden City Plaza
;       CITY:  Garden City
;       STATE:  New York
;       COUNTRY:  United States of America
;       ZIP:  11530
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/828,741B
;       FILING DATE:  26-MAR-1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DiGiglio, Frank S.
;       REGISTRATION NUMBER:  31,346
;       REFERENCE/DOCKET NUMBER:  10591
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (516) 742-4343
;       TELEFAX:  (516) 742-4366
;       TELEX:  230 901 SANS UR
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  495 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-828-741B-4

  Query Match             75.4%;  Score 513.5;  DB 4;  Length 495;
  Best Local Similarity   85.6%;  Pred. No. 2.3e-40;
  Matches  121;  Conservative    7;  Mismatches    9;  Indels    1;  Gaps    1;

Qy           1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLA 60
               |:|  ||: |: |:|||||||||:|||| || |:|:|| |||||||||||||  :|||
Db           5 MESQTLVFMSMSLLWVSGVYGEIVMSQSPDFQSVTPKEKVTITCRASQSIGSNIHWYQQK 64

Qy          61 WYQQKPDQSPKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
               |||||||||||||||||| |||||||:|||| |||||||||:|||||||||||||||   |:
Db          65 WYQQKPDQSPKFLIYWASTGESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSY 124

Qy         121  YTFGQGTKVEIK 132
                :|||  |||:|||
Db         125 FWFGGGTKLEIK 136


RESULT 14
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US-09-160-567-4
; Sequence 4, Application US/09160567
; Patent No. 6329179
;  GENERAL INFORMATION:
;     APPLICANT:  Koenigsen, Frank
;     APPLICANT:  Suess, Gabriele M.
;     APPLICANT:  Farlinton, David M.
;     APPLICANT:  Freutlein, Herbert R.
;     TITLE OF INVENTION:  CATALYTIC ANTIBODIES AND A METHOD OF
;     TITLE OF INVENTION:  PRODUCING SAME
;     NUMBER OF SEQUENCES:  14
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;       STREET:  400 Garden City Plaza
;       CITY:  Garden City
;       STATE:  New York
;       COUNTRY:  United States of America
;       ZIP:  11530
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/160,567
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/828,741
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DiGiglio, Frank S.
;       REGISTRATION NUMBER:  31,346
;       REFERENCE/DOCKET NUMBER:  10591
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (516) 742-4343
;       TELEFAX:  (516) 742-4366
;       TELEX:  230 901 SANS UR
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  495 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-160-567-4

  Query Match             75.4%;  Score 513.5;  DB 4;  Length 495;
  Best Local Similarity   85.6%;  Pred. No. 2.3e-40;
  Matches  121;  Conservative    7;  Mismatches    9;  Indels    1;  Gaps    1;

Qy           1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLA 60
               |:|  ||: |: |:|||||||||:|||| || |:|:|| |||||||||||||  :|||
Db           5 MESQTLVFMSMSLLWVSGVYGEIVMSQSPDFQSVTPKEKVTITCRASQSIGSNIHWYQQK 64

Qy          61 WYQQKPDQSPKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
               |||||||||||||||||| |||||||:|||| |||||||||:|||||||||||||||   |:
Db          65 WYQQKPDQSPKFLIYWASTGESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSY 124

Qy         121  YTFGQGTKVEIK 132
                :|||  |||:|||
Db         125 FWFGGGTKLEIK 136


RESULT 15
US-08-579-378A-2
; Sequence 2, Application US/08579378A
; Patent No. 5210171
;  GENERAL INFORMATION:
;     APPLICANT:  Ou, Man Sung
;     TITLE OF INVENTION:  Humanized Anti-Tac Antibody with
;     TITLE OF INVENTION:  L-Selectin
;     NUMBER OF SEQUENCES:  20
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
;       CITY:  San Francisco
;       STATE:  California
```

; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,478A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11824-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-478A-2

Query Match 75.4%; Score 512.5; DB 4; Length 133;
Best Local Similarity 72.9%; Pred. No. 6.7e-41;
Matches 97; Conservative 19; Mismatches 16; Indels 1; Gaps 1;

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Qy          1 MESQAQVLMPLLLWVSGACADIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSRTRKNYLA 60
              |:|| ||| |||||| | |||:|||| |||:|::: |::|||-|||||  ::|||
Db          1 MESQTQVLMFLLLWVSGACADIVMIQSPSSLAMSVGQKVIMSCKSSQSLLNSGNQKNYLA 60

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
              ||||||| |||:|:|||||||||||| ||||||||||||:|||:| |:| | |:
Db         61 WYQQKPGQSPKLLVYFASIRESGVPDRFIGSGSGTDFILTISSVQAEDLADYFCHQHYST 120

Qy        121 YTFGQGTKVEIK 132
                 |:| |||:|:|
Db        121 PTFGAGTKLELK 133
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Search completed: June 14, 2003, 15:14:09
Job time : 18.4034 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 13:02:04 ; Search time 1475.28 Seconds
(without alignments)
8570.448 Million cell updates/sec

Title: US-09-249-011B-5
Perfect score: 405
Sequence: 1 atgggttggaactgtatcat.....ccattgtcacggtctctca 405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: qb_ba:*
2: qb_htq:*
3: qb_in:*
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5: qb_ov:*
6: qb_pat:*
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8: qb_pl:*
9: qb_pr:*
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12: qb_sy:*
13: qb_un:*
14: qb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
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31: em_htq_inv:*
32: em_htq_other:*
33: em_htq_mus:*
34: em_htq_pln:*
35: em_htq_rod:*
36: em_htq_mam:*
37: em_htq_vrt:*
38: em_sy:*
39: em_htqo_hum:*
40: em_htqo_mus:*
41: em_htqo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	289.6	71.5	805	12	AF239196	AF239196 Synthetic
2	272.2	67.2	446	6	I08288	I08288 Sequence 4
3	272.2	67.2	462	10	S78361	S78361 ABI107 VH r
4	265.8	65.6	1767	6	E40699	E40699 Antihuman F
5	265.8	65.6	1768	6	E40700	E40700 Antihuman F
6	254.4	62.8	424	6	AR174947	AR174947 Sequence
7	254.6	62.8	452	6	AR144016	AR144016 Sequence
8	253.6	62.6	2071	6	E40080	E40080 Drug contai
9	253.6	62.6	2071	6	E40888	E40888 Humanized a
10	253.6	62.6	2071	6	E44434	E44434 Humanized a
11	253	62.5	4210	6	AX359931	AX359931 Sequence
12	253	62.5	4210	6	AX382145	AX382145 Sequence
13	252	62.2	2073	6	E40910	E40910 Humanized a
14	252	62.2	2073	6	E40911	E40911 Humanized a
15	251.4	62.1	405	9	HS1GHXX11	X65803 H.sapiens m
16	250.4	61.8	2073	6	E40912	E40912 Humanized a
17	249.8	61.7	474	9	AF397325	AF397325 Callithri
18	248.8	61.4	157	6	E40842	E40842 Drug contai
19	248.8	61.4	457	6	E40850	E40850 Humanized a
20	248.8	61.4	457	6	E43396	E43396 Humanized a
21	248.8	61.4	2077	6	E40855	E40855 Drug contai
22	248.8	61.4	2077	6	E40863	E40863 Humanized a
23	248.8	61.4	2077	6	E43409	E43409 Humanized a
24	248.2	61.3	433	6	AR024343	AR024343 Sequence
25	248.2	61.3	433	6	AR045196	AR045196 Sequence
26	248.2	61.3	433	6	BD011420	BD011420 Chimeric
27	248.2	61.3	433	6	E43890	E43890 Chimeric an
28	246.6	60.9	471	9	AF397351	AF397351 Callithri
29	245.6	60.6	2077	6	E43441	E43441 Humanized a
30	245	60.5	405	6	AR126855	AR126855 Sequence
31	245	60.5	405	6	I31950	I31950 Sequence 68
32	245	60.5	405	6	I78562	I78562 Sequence 68
33	245	60.5	405	6	I78617	I78617 Sequence 68
34	245	60.5	405	9	HSRGD114B	Z46348 Homo sapien
35	245	60.5	405	10	MUSIGHM195	M84098 Mus musculu
36	244.4	60.1	405	6	E16346	E16346 DNA encodin
37	244.4	60.1	1773	6	E14571	E14571 Mouse mRNA
38	244.4	60.1	1773	6	E40630	E40630 Antihuman F
39	241.8	59.7	414	9	AF062257	AF062257 Homo sapi
40	241.8	59.7	491	10	MUSANIVAJ	M37621 Mouse anti-
41	241.8	59.7	491	10	MUSIGBRS	M27799 Mouse Ig-ac
42	241.2	59.6	700	10	MUSIGBAQ	J00494 Mouse Ig-ac
43	241.2	59.6	706	10	MUSIGBMW	M25495 Mouse Ig-re
44	240.2	59.3	402	9	HSVHIB6	Z47222 H.sapiens m
45	240.2	59.3	406	10	MUSIGBMX	M28251 Mouse Ig-re

ALIGNMENTS

RESULT 1
AF239196
LOCUS AF239196 805 bp mRNA linear SYN 05-JUL-2002
DEFINITION Synthetic construct BCL1 lymphoma-derived single chain idiotype variable region mRNA, complete cds.
ACCESSION AF239196
VERSION AF239196.1 GI:8925814
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 805)
AUTHORS Schreurs,M.W.J., van der Berk,P.C.M., van Oers,M.H.J. and Kerstens,M.J.
TITLE Mouse BCL1 lymphoma-derived single chain antibody (scFv) sequence

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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 805)
  AUTHORS   Schreurs,M.W.J., van der Berk,P.C.M., van Oers,M.H.J. and
            Kerkstra,M.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-2000) Immunology, The Netherlands Cancer
            Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands
FEATURES             Location/Qualifiers
     source          1..805
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /clone
     source          join(10..417,464..792)
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /tissue_type="BCL1 lymphoma"
     CDS             10..792
                     /note="scFv"
                     /codon_start=1
                     /transl_table=11
                     /product="BCL1 lymphoma derived single chain Idiotypic
                     variable region"
                     /protein_id="AAF91417.1"
                     /db_xref="GI:8926615"
                     /translation="METDTLLLWVLLLWVPGSTGDIVLTQSPPSLAVSLGQRATISCRASE
                     GYEFTDYAMHWVRQSHAKSKLEWIGVISTYNGNTNYNQKFEGKATMTVDKSSSTAYMEL
                     ARLTSEDSAIYYCARVYGNYFDYWGQGTTLTVSSGGGGSGGGGSGGGGSQAVVTQESA
                     LTTSPGETVTLICRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSGS
                     LIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKVTVLG"
     sig_peptide     10..66
     misc_feature    67..417
                     /note="Region: heavy chain variable region"
     misc_feature    418..462
                     /note="Region: linker"
     misc_feature    463..792
                     /note="Region: lambda light chain V region"
BASE COUNT       206 a    191 c    206 g    202 t
ORIGIN

  Query Match             71.5%;  Score 289.6;  DB 12;  Length 805;
  Best Local Similarity   84.6%;  Pred. No. 8.6e-61;
  Matches  341;  Conservative    0;  Mismatches   64;  Indels    3;  Gaps    1;

Qy          1 ATGGGTCTGAACTGCATCATCTTCTTTCTGGTTACTGCAGGTACACAGGTGCAGCTGCAG 60
              ||||||| |||||||||||||||||||||||  | |||||||||||||||||||||||||
Db         10 ATGGGTTGGAGCTGTATCATCTTCTTCCTGGCAGTAACAGCTACAGGTGTCCACTCCCAG 69

Qy         61 GTTCAGCAGTCTGGTGCAGCTGGAGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTGTCC 120
              ||||||| |||||||||| |||||||  || ||||||  |||||||||| | |||
Db         70 GTTCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATTTCC 129

Qy        121 TGCAAAGCTTCTGGCTACACATTCACTGATTATGCTATACACTGGGTGAGACAGGCTCCT 180
              |||||  |||||||||||||||||||||||||||||||| || |||||||  ||| || |
Db        130 TGCAAGGCTTCTGGCTACACATTCACTGATTATGCTATGCACTGGGTGAAGCAGAGTCAT 189

Qy        181 GGACAGGGCCTTGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
              | | || | || |||||||||||| |||||| |  |||| ||| | ||||| |||||||
Db        190 GGAAAGAGTCTAGAGTGGATTGGAATTATTAGTTCTTACAATGGTGATACAAGCTACAAC 249

Qy        241 CAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 300
              ||||||||||||||||||||||||||||||||||||||||| || | ||||||||||||
Db        250 CAGAAGTTCAAGGGCAAGGCCACAATTACTGCAGACAAATCCTCCAGCACAGCCTACATG 309

Qy        301 CAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATACGGTAACT 360
              |||||||  |||| |||||| || | || | |||||||||||||||  | | |  |
Db        310 CAACTTGGCAGATTGACATCTGAAGATCTTGCCATCTATTTCTGTGCAAGA--GCAAGC 367

Qy        361 TATATGGACTACTGGGGTCAAGGTACCTTGGTCACCGTCTCCTCA 405
              |  | |||||||||||| |||| ||| | |||| ||||||||
Db        368 AACCTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 412


RESULT 3
S78361
locus       S78361                    402 bp    mRNA    linear   ROD 07-MAY-1993
DEFINITION  AB1167 VH region-chimeric mouse/human MAb against the human p55
            IL-2R heavy chain variable region gene, mRNA recombinant Partial,
            402 nt.
ACCESSION   S78361
VERSION     S78361.1  GI:243052
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Rose-John,S., Hilfiker-Kleiner,D., Barlow,D.A., Sabbil,K.,
            Deulbar,I., Shedd,D. and Zerler,B.
  TITLE     A chimeric mouse/human anti-IL-2 receptor antibody with enhanced
            biological activities
  JOURNAL   Mol. Immunol. 29 (1), 131-144 (1992)
  MEDLINE   92114886
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  FORMAT    1.1 (1187
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            entry [NCBI stbbsq 2.0] from the original journal article.
            This sequence comes from Fig1B.
FEATURES             Location/Qualifiers
     source          1..462
                     /organism="Mus sp."
                     /db_xref="taxon:10090"
     gene            1..462
                     /partial
                     /gene="Ab[illegible] V-region"
     CDS             61..462
                     /partial
                     /gene="AHI107 VH region"
                     /note="Shiseki; Accession/Human HAI against the human p55
                     IL-2R heavy chain variable region; this sequence comes
                     from Fig1B"
                     /codon_start=1
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                     /protein_id="AAP21910.1"
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BASE COUNT       122 a    112 c    118 g    110 t
ORIGIN

  Query Match             67.2%;  Score 272.2;  DB 16;  Length 462;
  Best Local Similarity   81.2%;  Pred. No. 2.8e-75;
  Matches  329;  Conservative    0;  Mismatches   74;  Indels    3;  Gaps    1;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACTACAGGTACAGGTGTGCACTCCCAG 60
              ||||| |||| |||||||||| |||||||||   | ||||||||| ||||||||||||||
Db         61 ATGGGCTGGAGCTGTATCATCCTCTTTCTGGCAGCAACAGCTACAAGTGTGCACTCCCAG 120

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120
              |||||||||  |||||||||| |||||||| ||||||||| |||||||||| | |||
Db        121 GTCCAGCTGCAGCAGTCTGGGCCTGAGCTGGTGAGGCCTGGGGCTCAGTGAAGATTTCC 180

Qy        121 TGCAAAGCTTCTGGCTACACATTCACTGATTATGCTATACACTGGGTGAAGCAGAGTCAT 180
              ||||| | |||||||||||||||||||||||||||| | || |||||| ||| || |
Db        181 TGCAAGGCTTCTGGGTACACATTCACTGATTATGCTCTCCACTGGGTGAAGCAGAGTCAT 240

Qy        181 GCAAAGAGCCTTGAGTGGATTGGAGTTATTAATACTGAAACTGGTGAGCCAACATATGCA 240
              | | || | || |||||||||||| |||||| |  |||| ||| | |||||| |||||||
Db        241 GTGACAGTGTCTAGAGTCGATCTAAGTATTAGTACTGCCTACTTGCAGATCAACAACCTC 300

Qy        241 TCAGAGGTTAAGGGCCGGTTCACCTTCTCTTTGGAAACATCTGCCAGTACTGCCTATCTG 300
              | || ||||||||||||||||||||||||||||||| || | |||||||||||||||||
Db        301 CGAGAGTTTAAGGACAGGTTTGTGTTCTCCATGGACACCTCTGTCAGCACGGCATATCTG 360

Qy        301 GAACTTAGTTCCTTGAGATCTGAGGATACGGCTGTGTATTACTGTGCAAGAGGGAGCAAC 360
              ||||||     ||| |||||| || | || | ||||||||||||||||   | | |
Db        361 GAACTTGCCAGATTGACATCTGAAGATTCTGCCATCTATTACTGTGCAAGA---GGAAGC 417

Qy        361 TATATGGACTACTGGGGCCAAGGTACCCTTGTCACCGTCTCCTCA 405
                | | ||||||||||| |||| || | |||| ||||||||
Db        418 AACCTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 462


RESULT 4
E40699
LOCUS       E40699                  1767 bp    DNA     linear   PAT 01-JAN-2002
DEFINITION  Antihuman Fas humanized antibody containing antirheumatic.
ACCESSION   E40699
VERSION     E40699.1  GI:18627288
KEYWORDS    JP 2000154149-A/70.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1767)
  AUTHORS   Soriwa,N., Hiroyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.
  TITLE     Antihuman Fas humanized antibody containing antirheumatic
  JOURNAL   Patent: JP 2000154149-A 70 06-JUN-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000154149-A/70
            PD   06-JUN-2000
            PF   17-SEP-1999 JP 1999264984
            PR
            IN   [illegible]SERIZAWA,HIDEKI;HIROYAMA,HAYATO;TAKAHASHI, [illegible]AKO;
            NAKAHARA,
            IN   SHIN YONEHARA
            [illegible]
            CC
            FH   Key             Location/Qualifiers
            FT   CDS             (1)..(1764)
            FT   mat_peptide     (58)..(1764)
            FT   sig_peptide     (1)..(57).
FEATURES             Location/Qualifiers
     source          1..1767
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       384 a    568 c    485 g    330 t
ORIGIN

  Query Match             65.6%;  Score 265.8;  DB 6;  Length 1767;
  Best Local Similarity   78.5%;  Pred. No. 3.6e-73;
  Matches  318;  Conservative    0;  Mismatches   87;  Indels    6;  Gaps    2;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACTACAGGTACAGGTGTGCACTCCCAG 60
              ||||| |||| |||||||||| |||||||||   | ||||||||| ||||||||||||||
Db          1 ATGGGCTGGAGCTGTATCATCCTCTTTCTGGCAGCAACAGCTACAAGTGTGCACTCCCAG 60

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120
              |||||||||  |||||||||| |||||||| ||||||||| |||||||||| | |||
Db         61 GTCCAGCTGCAGCAGTCTGGGCCTGAGCTGGTGAGGCCTGGGGCTCAGTGAAGATTTCC 120

Qy        121 TGCAAAGCTTCTGGCTACACATTCACTGATTATGCTATACACTGGGTGAAGCAGAGTCAT 180
              ||||| | |||||||||||||||||||||||||||| | || |||||| ||| || |
Db        121 TGCAAGGCTTCTGGGTACACATTCACTGATTATGCTCTCCACTGGGTGAAGCAGAGTCAT 180

Qy        181 GCAAAGAGCCTTGAGTGGATTGGAGTTATTAATACTGAAACTGGTGAGCCAACATATGCA 240
              | | || | || |||||||||||| |||||| |  |||| ||| | |||||| |||||||
Db        181 GTGACAGTGTCTAGAGTCGATCTAAGTATTAGTACTGCCTACTTGCAGATCAACAACCTC 240

Qy        241 TCAGAGGTTAAGGGCCGGTTCACCTTCTCTTTGGAAACATCTGCCAGTACTGCCTATCTG 300
              | || ||||||||||||||||||||||||||||||| || | |||||||||||||||||
Db        241 CGAGAGTTTAAGGACAGGTTTGTGTTCTCCATGGACACCTCTGTCAGCACGGCATATCTG 300

Qy        301 GAACTTAGTTCCTTGAGATCTGAGGATACGGCTGTGTATTACTGTGCAAGAGGGAGCAAC 360
              ||||||     ||| |||||| || | || | ||||||||||||||||   | | |
Db        301 GAACTTGCCAGATTGACATCTGAAGATTCTGCCATCTATTACTGTGCAAGA---GGAAGC 357

Qy        361 TATATGGACTACTGGGGCCAAGGTACCCTTGTCACCGTCTCCTCA 405
                | | ||||||||||| |||| || | |||| ||||||||
Db        358 AACCTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 402


RESULT 5
E40700
LOCUS       E40700                  1768 bp    DNA     linear   PAT 01-JAN-2002
DEFINITION  Antihuman Fas humanized antibody containing antirheumatic.
ACCESSION   E40700
VERSION     E40700.1  GI:18627289
KEYWORDS    JP 2000154149-A/71.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1768)
  AUTHORS   Soriwa,N., Hiroyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.
  TITLE     Antihuman Fas humanized antibody containing antirheumatic
  JOURNAL   Patent: JP 2000154149-A 71 06-JUN-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000154149-A/71
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            PD   06-JUN-2000
            PF   17-SEP-1999 JP 1999263984
            PR
            PI   NOBUKI SEKIZAWA,HIROSHI HAYASAMA,WATARU TAKAHASHI, PI   KAORI
            NAKAHARA,
            PI   SHIN YONEHARA
            PI   Abik-C-x-x-Arg[1,5]-Leu[1,5]-x-[2,3]-Phe-[2,3]-x-[2,3]-Leu[1,3]-
            Cys
            FH   Key             Location/Qualifiers
            FT   CDS             (1)..(1764)
            FT   mat_peptide     (58)..(1764)
            FT   sig_peptide     (1)..(57)
FEATURES             Location/Qualifiers
     source              1..1768
                         /organism="synthetic construct"
                         /db_xref="taxon:32630"
BASE COUNT       567 a    564 c    485 g    352 t
ORIGIN

  Query Match             65.6%;  Score 265.8;  DB 6;  Length 1768;
  Best Local Similarity   78.5%;  Pred. No. 4.6e-71;
  Matches  313;  Conservative    0;  Mismatches   87;  Indels    0;  Gaps    0;

Qy           1 ATGGGTTGGAACTGTATCATCTTCTTCTTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
               |||  |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db           1 ATGAAATGGAGCTGGGTCATTCTCTTCCTCCTGTCAGGAACTGCAGGTGTCCACTCTGAG 60

Qy          61 GTCCAGCTGCAGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120
               |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db          61 GTCTAGCTTCAGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGAGCCTCAGTGAAGGTTTCC 120

Qy         121 TGCAAAGCTTCTGGCTACACATTCACTGATTATGCTATACACTGGGTGAAGCAGGCCCCT 180
               |||| |||| || |||| |||||||| ||| ||| || ||||||| |||| | |
Db         121 TGCAAGGCTTCTGGATACACCTTCACTGACTATAATATGCATTGGGTGAAGCAGGCCCAT 180

Qy         181 GCACAGGGCCTTGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
               ||| || ||||||| |||| ||| |||| || |||| ||| | ||| |||||||
Db         181 GGAAAGAGCCTCGAATGGATGGGATATATTTATCCTTACAATGGTGGTACTGGCTACAAC 240

Qy         241 CAGAAGTTTAAGGGCAAGGCCACATTGACTGTAGACAAGTCGAGCAGCACAGCCTACATG 300
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Db         241 CAGAAGCTCAAGAGCAAGGCCACACTGACTGTCGACAATCCGAGCAGCACAGCCTACATG 300

Qy         301 GAACTCAGCTCCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCAAGAGCGGGCTAC 360
               || || ||   ||||||||||| || |||| |||| || |||| ||||||||     |
Db         301 GAGCTCATGAGCCTGAGATCTGAGGACACGGCAGTCTATTTCTGTGCAAGACGTCGGAGA 360

Qy         361 TA---TATGGACTACTGGGGTCAAGGTACCCTGGTCACCGTCTCCTCA 405
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Db         361 TATATATGGACTATGGGGTCAAGGAACCTCGTCACCGTCTCCTCA 418


RESULT 7
AR144016
LOCUS       AR144016                 451 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 11 from patent US 6210671.
ACCESSION   AR144016
VERSION     AR144016.1  GI:15105883
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Co,M.Suna.
  TITLE     Humanized antibodies reactive with L-selectin
  JOURNAL   Patent: US 6210671 A 11 03 APR 2001;
FEATURES             Location/Qualifiers
     source              1..451
                         /organism="unknown"
BASE COUNT       120 a    105 c    116 g    110 t
ORIGIN

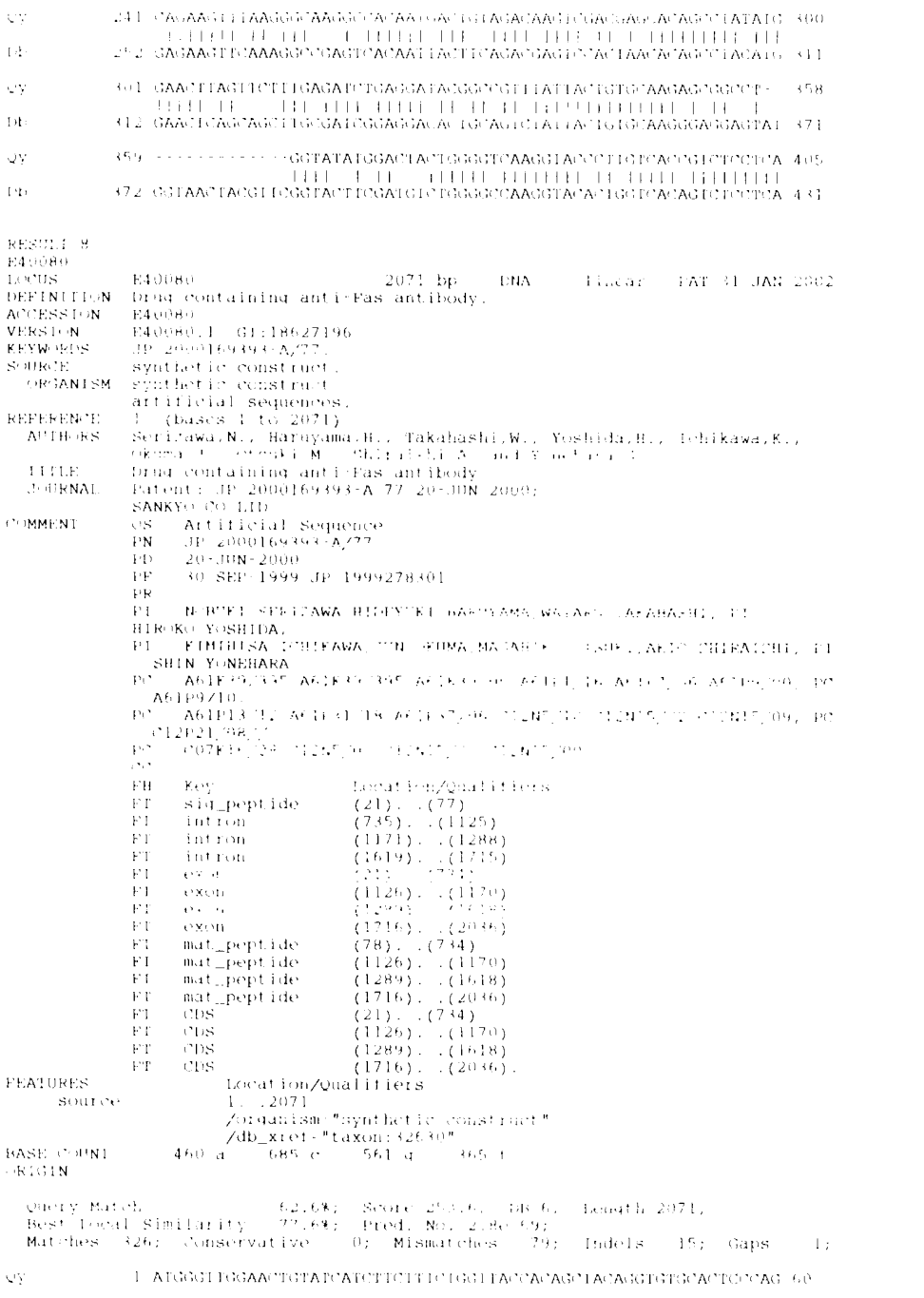
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  Best Local Similarity   77.6%;  Pred. No. 2.3e-69;
  Matches  426;  Conservative    0;  Mismatches   79;  Indels   15;  Gaps    1;

Qy           1 ATGGGTTGGAACTGTATCATCTTCTTCTTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
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Db          12 ATGGAATGGAGCTGGTATCATTCTCTTCCTGGTAGCAACAGCTACAGGTGTCCACTCCCAG 71

Qy          61 GTCCAGCTGCAGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120
               |||||||||| |||||||| |||| || |||| |||||||||||||| |||||||| |||
Db          72 GTCTAGCTGGTACAGTCTGGAGCTGAAGTCAAGAAGCCTGGGGCCTCAGTGAAGGTATCC 131

Qy         121 TGCAAAGCTTCTGGCTACACATTCACTGATTATGCTATACACTGGGTGAAGCAGGCCCCT 180
               |||| |||| || |||||||||||   |||| ||| || |||||||||||||| |||
Db         132 TGCAAGGCATCTGGTTACACCTTCACTGACTATAATATGCACTGGGTGAAGCAGACCCCT 191

Qy         181 GCACAGGGCCTTGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
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Db         192 GGACCAAGGACTCGAGTGGATTGGATATATTTATCCTTACAATGGTGGTACTGACTACAAT 251
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RESULT 8
E40080
LOCUS E40080 2071 bp DNA linear PAT 31-JAN-2002
DEFINITION Drug containing anti-Fas antibody.
ACCESSION E40080
VERSION E40080.1 GI:18627196
KEYWORDS JP 2000169393-A/77.
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 2071)
AUTHORS Serizawa,N., Haruyama,H., Takahashi,W., Yoshida,H., Ishikawa,K., Okuma,T., Ozawa,M., Shiraishi,A. and Tamaki,K.
TITLE Drug containing anti-Fas antibody
JOURNAL Patent: JP 2000169393-A 77 20-JUN-2000;
SANKYO CO LTD
COMMENT OS Artificial Sequence
PN JP 2000169393-A/77
PD 20-JUN-2000
PF 30-SEP-1999 JP 1999278301
PR
PI NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI,
HIROKO YOSHIDA,
PI FUMIHISA ISHIKAWA,TOMOKO OKUMA,MASAKO OZAWA,AKIO SHIRAISHI,
SHIN YONEHARA
PO A61K39/395,A61K39/395,A61K39/00,A61K47/26,A61K47/48,
A61P9/10,
PO A61P13/12,A61P13/12,A61P35/00,C12N5/10,C12N15/09,
C12P21/08,
PO C07K16/28,C12N5/10,C12N5/12,C12N15/09,
FH Key Location/Qualifiers
FT sig_peptide (21)..(77)
FT intron (735)..(1125)
FT intron (1171)..(1288)
FT intron (1619)..(1715)
FT exon (21)..(734)
FT exon (1126)..(1170)
FT exon (1289)..(1618)
FT exon (1716)..(2036)
FT mat_peptide (78)..(734)
FT mat_peptide (1126)..(1170)
FT mat_peptide (1289)..(1618)
FT mat_peptide (1716)..(2036)
FT CDS (21)..(734)
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FT CDS (1716)..(2036).
FEATURES Location/Qualifiers
source 1..2071
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 460 a 685 c 561 g 365 t
ORIGIN

Query Match 62.6%; Score 2533.6; DB 6; Length 2071;
Best Local Similarity 77.6%; Prod. No. 2.2e-69;
Matches 826; Conservative 0; Mismatches 79; Indels 15; Gaps 1;

RESULT 9
E40888
LOCUS E40888 2071 bp DNA linear PAT 31-JAN-2002
DEFINITION Humanized anti-Fas antibody.
ACCESSION E40888
VERSION E40888.1 GI:18627465
KEYWORDS JP 2000166574-A/77.
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 2071)
AUTHORS Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,K.
TITLE Humanized anti-Fas antibody
JOURNAL Patent: JP 2000166574-A/77 20-JUN-2000;
SANKYO CO LTD
COMMENT OS Artificial Sequence
PN JP 2000166574-A/77
PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275441
PR
PI NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO TAMAKI
PO C07K16/18,
PO C12N5/10
FH Key Location/Qualifiers
FT sig_peptide (21)..(77)
FT intron (735)..(1125)
FT intron (1171)..(1288)
FT intron (1619)..(1715)
FT exon (21)..(734)
FT exon (1126)..(1170)
FT exon (1289)..(1618)
FT exon (1716)..(2036)
FT mat_peptide (78)..(734)
FT mat_peptide (1126)..(1170)
FT mat_peptide (1289)..(1618)
FT mat_peptide (1716)..(2036)
FT CDS (21)..(734)
FT CDS (1126)..(1170)
FT CDS (1289)..(1618)
FT CDS (1716)..(2036).
FEATURES Location/Qualifiers
source 1..2071

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                     /organism "synthetic construct"
                     /db_xref "taxon:32630"
BASE COUNT       460 a    685 c    561 g    365 t
ORIGIN

  Query Match          62.6%;  Score 253.6;  DB 6;  Length 2071;
  Best Local Similarity   77.6%;  Prod. No. 2.8e-69;
  Matches  326;  Conservative    0;  Mismatches   79;  Indels   15;  Gaps    1;

Qy           1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTACCACAGCTACAGGTGTCCACTCCCAG 60
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Db          21 ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCTCAG 80

Qy          61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 120
               ||||| |||||||||||||||||||||| |||||||||||   |||||||||||||||
Db          81 GTCCAACTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 140

Qy         121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACATGGGGTGAGACAGGCTCCT 180
               ||||| ||||| |||||||| ||||     ||    || |||||||| | |||||| |||
Db         141 TGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCAGTGGGCTAAAACAGGCCCCT 200

Qy         181 GGACAAGGGCTTGAGTGGATTGGAGCTATTAATATTTACTATGATAATACAAACTACAAC 240
               |||||||||| |||||||| |||  ||| ||  ||   ||    |||| ||||||||
Db         201 GGACAGGGCCTTGAGTGGATGGGAGCATTGATCCTTCTGATAGCTATACTAACTACAAT 260

Qy         241 CAGAAGTTTAAGGGCAAGGCCACATTGACTGTAGACAAGTCGACGAGCACAGCCTATATG 300
               || |||| ||||||||||||||| ||||||||||| || || ||||||||||| |||
Db         261 CAAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCACTAGCACAGCCTACATG 320

Qy         301 GAACTTAGCTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA--------- 351
               || || ||     |||||||||||| |||| || |||||||||||||||
Db         321 GAGCTGAGGAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCAAGAAATAGGGAC 380

Qy         352        GCGGCCTGGTATATGGACTACTGGGGCCAAGGTACCCTTGTCACCGTCTCCTCA 405
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Db         381 TATAGTAACAACTGGTACTTCGATGTCTGGGGCGAAGGGACCACGGTCACCGTCTCCTCA 440


RESULT 10
B43434
LOCUS       B43434                  2071 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Humanized anti-Fas antibody.
ACCESSION   B43434
VERSION     B43434.1  GI:18627700
KEYWORDS    JP 2000166574-A/77.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 2071)
  AUTHORS   Takahashi,W., Haruyama,H. and Serizawa,N.
  TITLE     Humanized anti-Fas antibody
  JOURNAL   Patent: JP 2000166574-A 77 20-JUN-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            DN   JP 2000166574-A/77
            PD   20-JUN-2000
            PF   24-SEP-1999 JP 1999270440
            PR
            PI   WATABE,TAKAHASHI,HIDEYUKI,HARUYAMA,NOBUKI,SERIZAWA,NO
            XX   ANTIBODY TO HUMAN FAS ANTIGEN, USEFUL FOR
            AGONIST ACTIVITY.
            PC   C07K16/28; C12N15/09; C12N5/10; C12P21/08;
            PC   C12R1:91).
            PC   C12N15/09-ZNA,C12N5/10-ZNA,C12P21/08-ZNA
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FEATURES             Location/Qualifiers
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                     /organism "synthetic construct"
                     /db_xref "taxon:32630"
BASE COUNT       460 a    685 c    561 g    365 t
ORIGIN

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  Best Local Similarity   77.6%;  Prod. No. 2.8e-69;
  Matches  326;  Conservative    0;  Mismatches   79;  Indels   15;  Gaps    1;

Qy           1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTACCACAGCTACAGGTGTCCACTCCCAG 60
               ||||| |||| |||||||||| |||| |||  | |||||||||||||| |||| |||
Db          21 ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCTCAG 80

Qy          61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 120
               ||||| |||||||||||||||||||||| |||||||||||   |||||||||||||||
Db          81 GTCCAACTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 140

Qy         121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACATGGGGTGAGACAGGCTCCT 180
               ||||| ||||| |||||||| ||||     ||    || |||||||| | |||||| |||
Db         141 TGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCAGTGGGCTAAAACAGGCCCCT 200

Qy         181 GGACAAGGGCTTGAGTGGATTGGAGCTATTAATATTTACTATGATAATACAAACTACAAC 240
               |||||||||| |||||||| |||  ||| ||  ||   ||    |||| ||||||||
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Qy         241 CAGAAGTTTAAGGGCAAGGCCACATTGACTGTAGACAAGTCGACGAGCACAGCCTATATG 300
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Db         261 CAAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCACTAGCACAGCCTACATG 320

Qy         301 GAACTTAGCTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA--------- 351
               || || ||     |||||||||||| |||| || |||||||||||||||
Db         321 GAGCTGAGGAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCAAGAAATAGGGAC 380

Qy         352        GCGGCCTGGTATATGGACTACTGGGGCCAAGGTACCCTTGTCACCGTCTCCTCA 405
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Db         381 TATAGTAACAACTGGTACTTCGATGTCTGGGGCGAAGGGACCACGGTCACCGTCTCCTCA 440


RESULT 11
AX359931
LOCUS       AX359931                4210 bp    DNA     linear   PAT 14-FEB-2002
DEFINITION  Sequence 5 from Patent WO0202783.
ACCESSION   AX359931
VERSION     AX359931.1  GI:18625570
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Block,G.L.
  TITLE     Expression vectors
  JOURNAL   Patent: WO 0202783 A 5 10-JAN-2002;
            Gala Design, Inc. (US)
FEATURES             Location/Qualifiers
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                     /organism "synthetic construct"
                     /db_xref "taxon:32630"
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ORIGIN

  Query Match          62.5%;  Score 253;  DB 6;  Length 4210;
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  Best Local Similarity   76.5%;  Pred. No. 4.8e-69;
  Matches  310;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

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Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
Db        912 GTCCAGCTGGTCCAATCAGGGGCTGAAGTCAAGAAACCTGGGTCATCAGTGAAGGTCTCC 971

Qy        121 TGCAAAGCTTCTGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGCTCCT 180
Db        972 TGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGCTGCACTGGGTCAGGCAGGCACCT 1031

Qy        181 GGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
Db       1032 GGACAGGGTCTGGAATGGATTGGATACATTAATCCTAGGAATGATTATACTGAGTACAAT 1091

Qy        241 CAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTATATG 300
Db       1092 CAGAACTTCAAGGACAAGGCCACAATAACTGCAGACGAATCCACCAATACAGCCTACATG 1151

Qy        301 GAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGCCTGG 360
Db       1152 CAGCTGAGCAGCCTGAGGTCTGA[illegible]ATTTATTTTTGT[illegible]AAGAAGGGATATT 1211

Qy        361 TATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
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RESULT 12
AX382145
LOCUS       AX382145                4210 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 5 from Patent WO0202738.
ACCESSION   AX382145
VERSION     AX382145.1  GI:19576954
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bremel,R.D., Miller,L.U., Bleck,G.T. and York,D.
  TITLE     Host cells containing multiple integrating vectors
  JOURNAL   Patent: WO 0202738-A 5 10-JAN-2002;
            Gala Design, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..4210
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT     1053 a   1185 c   1037 g    935 t
ORIGIN

  Query Match             62.5%;  Score 253;  DB 6;  Length 4210;
  Best Local Similarity   76.5%;  Pred. No. 4.8e-69;
  Matches  310;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
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Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
Db        912 GTCCAGCTGGTCCAATCAGGGGCTGAAGTCAAGAAACCTGGGTCATCAGTGAAGGTCTCC 971

Qy        121 TGCAAAGCTTCTGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGCTCCT 180
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Qy        181 GGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
Db       1032 GGACAGGGTCTGGAATGGATTGGATACATTAATCCTAGGAATGATTATACTGAGTACAAT 1091

Qy        241 CAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTATATG 300
Db       1092 CAGAACTTCAAGGACAAGGCCACAATAACTGCAGACGAATCCACCAATACAGCCTACATG 1151

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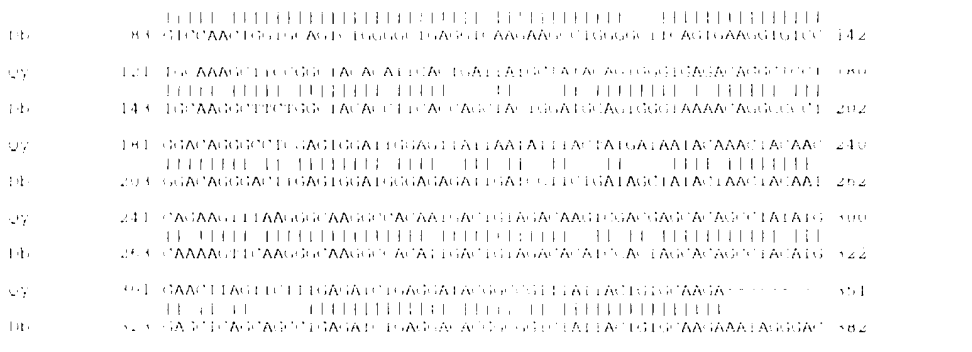
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RESULT 13
E40910
LOCUS       E40910                  2073 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Humanized anti-Fas antibody.
ACCESSION   E40910
VERSION     E40910.1  GI:18627487
KEYWORDS    JP 2000166574-A/99.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 2073)
  AUTHORS   [illegible],N., Haruyama,H., Nakahara,K. and Tamaki,T.
  TITLE     Humanized anti-Fas antibody
  JOURNAL   Patent: JP 2000166574-A 99 20-JUN-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000166574-A/99
            PD   20-JUN-2000
            PF   29-SEP-1999 JP 1999275442
            PR
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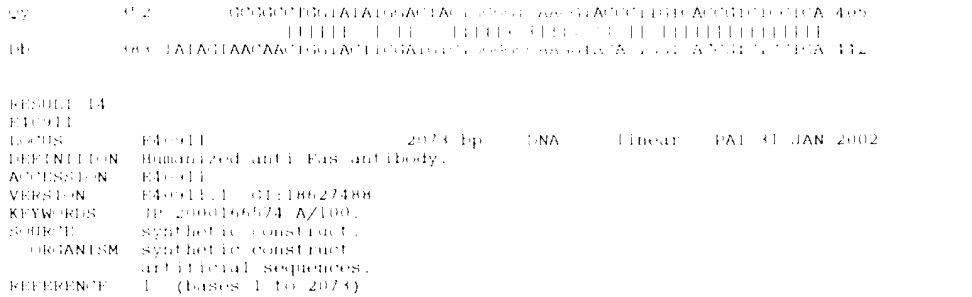
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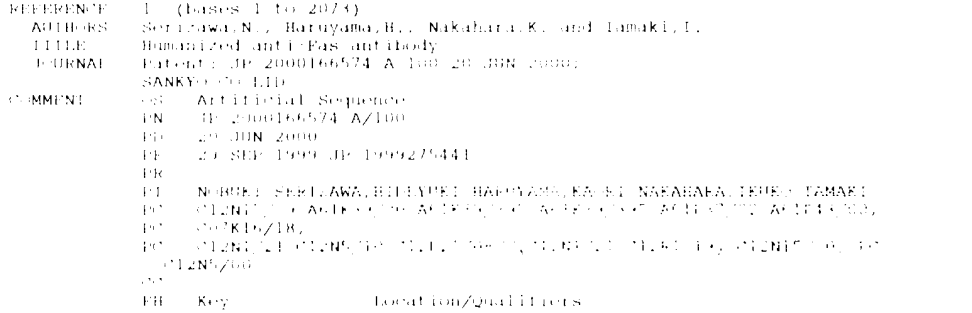
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RESULT 14
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LOCUS E40911 2073 bp DNA linear PAT 31 JAN 2002
DEFINITION Humanized anti-Fas antibody.
ACCESSION E40911
VERSION E40911.1 GI:18627488
KEYWORDS JP 2000166574-A/100.
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 2073)
AUTHORS Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
TITLE Humanized anti-Fas antibody
JOURNAL Patent: JP 2000166574-A 100 20-JUN-2000;
SANKYO CO LTD
COMMENT os Artificial Sequence
PN JP 2000166574-A/100
PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275441
PR
PI Nobuki Serizawa,Hideyuki Haruyama,Ken-ichi Nakahara,Ikuo Tamaki
DC C12N15/09; C12N5/10; C12N15/13; C12N15/62; C12P21/02;
DC C07K16/18;
DC C12N15/24 C12N5/10 C12N15/13 C12N15/62 C12P21/02 C07K16/18
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BASE COUNT 454 a 686 c 558 g 366 t
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Query Match 52.2%; Score 252; DB 6; Length 2073;
Best Local Similarity 77.4%; Pred. No. 9e-69;
Matches 526; Conservative 0; Mismatches 80; Indels 152; Gaps 3;



RESULT 15
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DEFINITION H.sapiens mRNA for XLA IG heavy chain VDJ region (LE 1-9).
ACCESSION X65093 S59756
VERSION X65093.1 GI:955090
KEYWORDS diversity region; Ig heavy chain; immunoglobulin; joining region;
variable region.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS Schiff,C.
TITLE Direct Submission
JOURNAL Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de
Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
REFERENCE 2 (bases 1 to 405)
AUTHORS Milili,M., le Doist,F., de Saint-Basile,G., Fischer,A.,
Fougereau,M. and Schiff,C.
TITLE Bone marrow cells in X linked agammaglobulinemia express
pre-B specific genes (lambda-like and V pre-B) and present
immunoglobulin V-D-J gene usage strongly biased to a fetal-like
repertoire
JOURNAL J. Clin. Invest. 91 (4), 1616-1629 (1993)
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Qy 61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
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Qy 121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACACTGGGTGAGACAGGCTCCT 180
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Qy 181 GGACAGGGCCTCGAGTGGATGGGATTATTAATATTTACTATGATAAATACAAACTACAAC 240
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Qy 241 CAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCCGCGAGCACAGCCTATATG 300
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Qy 301 GAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGCCTGG 360
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Qy 361 TATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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35	224.4	55.4	567	10	BE287568	BE287568 601097404
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40	224.2	55.4	1093	12	BF974290	BF974290 602243946
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43	224	55.3	724	13	BG962137	BG962137 602829092
44	223.4	55.2	880	14	BQ707384	BQ707384 AGENCOURT
45	223.2	55.1	784	13	BM007990	BM007990 603617726

ALIGNMENTS

RESULT 1
BQ965088
LOCUS BQ965088 748 bp mRNA linear EST 12-JUN-2001
DEFINITION 602829160F1 NIH_MGC_24 Mus musculus cDNA clone IMAGE:4983974 5', mRNA sequence.
ACCESSION BQ965088
VERSION BQ965088.1 GI:14352725
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 748)
AUTHORS [illegible]
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRAM10989 row: q column: 15
High quality sequence stop: 716.
FEATURES Location/Qualifiers
source 1..748

/organism "Mus musculus"
/strain "FVB/N"
/db_xref "taxon:10090"
/clone "IMAGE:4983674"
/clone_lib "NCI_CGAP_Co24"
/lab_host "DH10B (T1 phage-resistant)"
/note "organ: colon; Vector: pCMV-SPORT6; Site_1: Not I;
Site_2: Sal I; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 195 a 186 c 189 g 168 t
ORIGIN

Query Match 69.6%; Score 282; DB 13; Length 738;
Best Local Similarity 82.1%; Pred. No. 5.2e-79;
Matches 440; Conservative 0; Mismatches 65; Indels 9; Gaps 1;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
Db 40 ATGGGTAGGAGCTGTATCATCTTCTTCTGGTAGCAACAGCTACAGGTGTACACTCCCAG 99

Qy 61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
Db 100 GTCCAGCTGCAGCAGTCTGGGCCTGAGCTGGTGAGGCCTGGGGCTCTCAGTGAAGATCTCC 159

Qy 121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGCTCCT 180
Db 160 TGCAAGGGTTCCGGCTACACATTCACTGATTATGCTATACACTGGGTGAAGCAGAGTCAT 219

Qy 181 GGACAGGGCCTCGAGTGGATTGGATGGATTAATACTTACTATGATAATACAAACTACAAC 240
Db 220 GCAAAGAGTCTAGAGTGGATTGGAGTTATTAATACTTACTATGGTAAAACAAACTGCAAC 279

Qy 241 CAGAAGTTTAAGGGCAAGGCCACAATCACTGTAGACAAGTCGACGAGCACAGCCTATATG 300
Db 280 CAGAAGTTTGAGGGCAAGGCCACAATCACTGTAGACAAATCCTCCAGCACAGCCTATATG 339

Qy 301 CAACTTAGTAGTCTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA---- - -- 351
Db 340 CAACTTGCAGATTGACAGCTGAGGATCTGGCCATCTATTACTGTGCAAGATTATTGTGGG 399

Qy 352 GGGGA-TGGTATAIGGACTACTGGGGCCAAGGTACCTTGGTCACCGTCTCCTCA 405
Db 400 GGAAACTATGGTGTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 453

RESULT 2
BG961255
LOCUS BG961255 633 bp mRNA linear EST 12-JUN-2001
DEFINITION 602826478F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4981242 5',
mRNA sequence.
ACCESSION BG961255
VERSION BG961255.1 GI:14349392
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 633)
AUTHORS NIH MGC http://www.ncbi.nlm.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9082 row: e column: 19
High-quality sequence stop: 617.

FEATURES Location/Qualifiers
source 1..633
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4981242"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="organ: colon; Vector: pCMV-SPORT6; Site_1: Not I;
Site_2: Sal I; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 160 a 153 c 164 g 157 t
ORIGIN

Query Match 62.3%; Score 252.2; DB 13; Length 633;
Best Local Similarity 83.7%; Pred. No. 1.7e-69;
Matches 309; Conservative 0; Mismatches 58; Indels 2; Gaps 2;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTACC ACAGCTACAGGTGTGCACTCCCA 59
Db 40 ATGGGTAGGAGCTGTATCATCTTCTTCTGGTAGCAACAGCTACAGGTGTACACTCCCA 99

Qy 60 GGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 119
Db 100 GGTCCAGCTGCAGCAGTCTGGGCCTGAACTGGTGAGGCCTGGGGCTCTCAGTGAAGATTTCC 159

Qy 120 CTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGCTCCT 179
Db 160 CTGCAAGGGTTCCGGCTACACATTCACTGATTATGCTTTACACTGGGTGAAGCAGAGTCA 219

Qy 180 TGGACAGGGCCTCGAGTGGA-TGGATGGATTAATAATACTTACTATGATAATACAAACTACA 238
Db 220 TGGAAAGAGTCTGGAGTGGACTTGGAATTATTAGTACTTACTATGGCAATACAAGTTACA 279

Qy 239 ACCACAAGTTTAAGGGCAAGGCCACAATCACTGTAGACAAGTCGACGAGCACAGCCTATA 298
Db 280 ATCAGAAGTTTAAGGGCAAGGCCCCAATCACTGTAGACAAATCTTCCAGCACAGCCTATA 339

Qy 299 TGCAACTTAGTAGTCTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGGGGGAAG 358
Db 340 TGCAACTTGCAGATTGACAGCTGAGGATCTGGCCATCTATTACTGTGCAAGAGGGGAAG 399

Qy 359 GGTATATGGC 367
Db 400 CGTATGGGC 408

RESULT 3
BG968682
LOCUS BG968682 690 bp mRNA linear EST 12-JUN-2001
DEFINITION 602836513F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4990947 5',
mRNA sequence.
ACCESSION BG968682
VERSION BG968682.1 GI:14356406
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 690)
AUTHORS NIH MGC http://www.ncbi.nlm.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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            Plate: LLAM11007  row: j  column: 04
            High quality sequence stop: 679.
FEATURES             Location/Qualifiers
     source          1..690
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4990947"
                     /clone_lib="NCI_CGAP_Co24"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT       173 a    192 c    170 g    155 t
ORIGIN

  Query Match             59.7%;  Score 241.8;  DB 13;  Length 690;
  Best Local Similarity   76.2%;  Pred. No. 3.8e-66;
  Matches  313;  Conservative    0;  Mismatches   92;  Indels    6;  Gaps    1;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTCCACTCCCAG 60
              ||||| |||| |||||||||| |||| |||| | ||||||||||||||| ||||||||||
Db         84 ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCCCAG 93

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
              ||||| ||| |||| |||||||||| || ||||||||||   |||||||| |||||
Db         94 GTCCAACTGCAGCAGCCTGGGGCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGTTGTCC 153

Qy        121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAAGCAGAGGCCT 213
              ||||| |||| |||||||| |||| | ||   || || ||||||| ||||   |||
Db        154 TGCAAGGCTTCTGGCTACACCTTCACCAACTACTGGATGCACTGGGTGAAACAGAGGCCT 213

Qy        181 GGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
              ||||| |||| |||||||||| |||||||  | |   || || ||| ||||||||
Db        214 GGACAAGGCCTTGAGTGGATTGGAAATATTAATCCTAATAGTGGTAGTACTAACTACAAT 273

Qy        241 CAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACCAGCACAGCCTATATG 300
              ||||||| ||| |||||||||| |||||||||| |  ||  | ||||||||| |||
Db        274 GACAAGTTCAAGAGCAAGGCCACATTGACTGTAGATAAATCCTCCAGCACAGCCTACATG 333

Qy        301 GAACTTAGCTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCG------ 354
              | || ||    | | ||||| ||| |  || || |||||||||| ||| | |
Db        334 CAGCTCAGCAGCCTCACATCTGCGGACTCTGCGGTCTATTACTGTACAATAAGGTTGCTA 393

Qy        355 GCCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
              |  | ||||||||||||||||||||||||| |||   ||||||||||||||||
Db        394 CGTTATTCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 444


RESULT 4
BG966397                                819 bp    mRNA    linear   EST 12-JUN-2001
LOCUS       BG966397
DEFINITION  602832896F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4987631 5',
            mRNA sequence.
ACCESSION   BG966397
VERSION     BG966397.1  GI:14354034
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 819)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cqapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10998  row: o  column: 24
            High quality sequence stop: 766.
FEATURES             Location/Qualifiers
     source          1..819
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4987631"
                     /clone_lib="NCI_CGAP_Co24"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT       206 a    229 c    199 g    185 t
ORIGIN

  Query Match             58.9%;  Score 238.6;  DB 13;  Length 819;
  Best Local Similarity   75.7%;  Pred. No. 4.4e-65;
  Matches  311;  Conservative    0;  Mismatches   94;  Indels    6;  Gaps    1;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTCCACTCCCAG 60
              ||||| |||| |||||||||| |||| |||| | ||||||||||||||| ||||||||||
Db         25 ATGGGATGGAGCTATATCATCCTCTTTTGGTAGCAACAGCTACAGGTGTCCACTCCCAG 84

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
              ||||| ||| |||| |||||||||| || ||||||||||   |||||||| |||||
Db         85 GTCCAACTGCAGCAGCCTGGGGCTGAACTGGTGAAGCCTGGGACTTCAGTGAAGTTGTCC 144

Qy        121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAAGCAGAGGCCT 213
              ||||| |||| |||||||| |||| | ||   || || ||||||| ||||   |||
Db        145 TGCAAGGCTTCTGGCTACACCTTCACCAACTACTATATGTATGGGTGAAGCAGAGGCCT 204

Qy        181 GGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
              ||||| |||| |||||||||| |  |||||||  |  | |||  |   || || |  ||
Db        205 GGACAAGGCCTTGAGTGGATTGGGGGGATTAATCCTACCAATGGTGGCAACTAATTTTAAT 264

Qy        241 CAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACCAGCACAGCCTATATG 300
              ||||||| ||| |||||||||| |||||||||| ||  | ||||||||| | |||
Db        265 GAGAAGTTCAAGAACAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCCACATG 324

Qy        301 GAACTTAGCTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCG------ 354
              |||| ||    ||| |||||||||  | || || |||||||||| |||| |
Db        325 CAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTACAAGAGGAGTAAC 384

Qy        355 GCCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
              |  | ||||||||||||||||||||||||| |||   ||||||||||||||||
Db        385 TTCGATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 435


RESULT 5
BQ706192                                922 bp    mRNA    linear   EST 16-JUL-2002
LOCUS       BQ706192
DEFINITION  AGENCOURT_8354853 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281087
            5', mRNA sequence.
ACCESSION   BQ706192
VERSION     BQ706192.1  GI:21845091
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 922)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cqapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```

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            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2473  row: e  column: 23
            High quality sequence stop: 553.
FEATURES             Location/Qualifiers
     source          1..922
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                     /db_xref="taxon:10090"
                     /clone="IMAGE:6280092"
                     /clone_lib="NIH MGC 114"
                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: spleen; Vector: pCMV-SPORT6; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo dT priming, Directionally cloned
                     into EcoRI/XhoI site; Seq primers: 5' vector 5' GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT       195 a    297 c    260 g    170 t
ORIGIN

  Query Match             58.9%;  Score 238.6;  DB 14;  Length 922;
  Best Local Similarity   74.3%;  Pred. No. 4.7e-65;
  Matches  301;  Conservative    9;  Mismatches  104;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGGTACAGGTGTGCACTCCCAG 60
              |||| |||| ||| |   || ||||| |||  |  |||||||||||||| || ||||||
Db         84 ATGGACTGGACCTGGAGGTTCCTCTTTGTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAG 93

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
              |||| |||||||||||||||||||||||||||||||||||||||||||  ||| |||||| ||
Db         94 GTCCACTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCC 153

Qy        121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACATGGGGTGAGACAGGCTCCT 180
              ||.|| |||||.||   ||| ||||   |||||||||    |||||| |||||| |||
Db        154 TGCAAGGCTTCTGGATACACCTTCAGAAATTATGCTATCAGTTGGGTGCGACAGGCCCCT 213

Qy        181 GGACAGGGGCTTGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
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Db        214 GGACAAGGGCTTGAGTGGATGGGAATCATCCCTATTTTTGGTACAACAACTACGCA 273

Qy        241 CAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTATATG 300
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Db        274 CAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACATG 333

Qy        301 GAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGG 355
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Db        334 GAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTATTGTGCGAGAGAGTGGGAT 393

Qy        301 TATATGGACTACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCA 345
              | | ||   |||||| || || ||  | ||||||||||| |||
Db        394 CTCTGGGATATCTGGGGCCAGGGAACAATGGTCACCGTCTCTTCA 438
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RESULT 6
BI249216
LOCUS       BI249216                 770 bp    mRNA    linear   EST 17-JUL-2001
DEFINITION  602994779F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5150778 5',
            mRNA sequence.
ACCESSION   BI249216
VERSION     BI249216.1  GI:14796464
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 770)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
```

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COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11472  row: m  column: 19
            High quality sequence start: 4
            High quality sequence stop: 769.
FEATURES             Location/Qualifiers
     source          1..770
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5150778"
                     /clone_lib="NCI_CGAP_Mam5"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="7 months"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Robin Humphreys,
                     NIH"
BASE COUNT       188 a    216 c    193 g    173 t
ORIGIN

  Query Match             58.1%;  Score 235.4;  DB 13;  Length 770;
  Best Local Similarity   75.2%;  Pred. No. 4.5e-64;
  Matches  309;  Conservative    0;  Mismatches   96;  Indels    6;  Gaps    1;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGGTACAGGTGTGCACTCCCAG 60
              ||||| |||| || ||||||| |||  |||  | |||||||||||||| |||||||||
Db         35 ATGGGATGGAGCTCTATCATCCTCTTCTGGTAGCAACAGGTACAGGTGTCCACTCCCAG 94

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
              ||||| |||  |||| |||| | || || || ||  |||||||| |||||||| ||||
Db         95 GTCCAACTGCAGCAGCTGGGGTCTGATGCTGGTGAAGCCTGGGGCCTCAGTGAAGCTGTCC 154

Qy        121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACATGGGGTGAGACAGGCTCCT 180
              ||||| ||||| |||||||| ||||    ||    |||| ||| || |||   |||
Db        155 TGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATACATGGGGTGAAACAGAGGCCT 214

Qy        181 GGACAGGGGCTTGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
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Db        215 GGAGAAGGCTTGAGTGGATTGGAGAGATTCATCCTAATAGTGGTACTAACTACAACGAG 274

Qy        241 CAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTATATG 300
              |||||| |||||||||||| |||| ||||||||||  || | ||||||||| |||
Db        275 GAGAAATTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCGAGCACAGCCTACATG 334

Qy        301 GAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGG 355
              || || ||     ||| |||||||| | || || ||||||||||||||| ||
Db        335 GAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGGGGTATAT 394

Qy        356 CCTGGTCATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
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Db        395 AGCTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCCTCA 445
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RESULT 7
BQ929209
LOCUS       BQ929209                 933 bp    mRNA    linear   EST 29-AUG-2002
DEFINITION  AGENCOURT_8953380 NCI_CGAP_Co24 Mus musculus cDNA clone
            IMAGE:6477483 5', mRNA sequence.
ACCESSION   BQ929209
VERSION     BQ929209.1  GI:22344240
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 933)
  AUTHORS   NIH MGC http://www.mgc.ncbi.nlm.nih.gov/
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM4019  row: d  column: 24
            High quality sequence stop: 546.
FEATURES             Location/Qualifiers
     source          1..933
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4015172"
                     /clone_lib="NCI_CGAP_Lu30"
                     /lab_host="DH10B (T1 phage resistant)"
                     /note="Organ: colon; Vector: pCMV SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: oligo dT
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      223 a    261 c    236 g    211 t      2 others
ORIGIN

  Query Match             57.9%;  Score 234.6;  DB 14;  Length 933;
  Best Local Similarity   75.1%;  Pred. No. 9e-64;
  Matches  310;  Conservative    0;  Mismatches   94;  Indels    9;  Gaps    1;

Qy          2 IGSGIEGGAAVTGTAFCAFCTTCTTTCTGGTTACCACACCTACACCCTCTGCACTTCCCACCC 61
              ||||| |||| || ||||||| |||| |||| | |||||||||||||| ||||||||||
Db          1 TGGGATGGAGCTATATCATCCCTCTTTTGGTAGCAACAGCTACAGGTGTCCACTCCCAGG 60

Qy         62 TCCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCCT 121
              |||| |||  |||| ||||||||||  || ||||||||||  |||||||||| ||||||
Db         61 TCCAACTGCAGCAGCCTGGGGCTGAACTGGTGAAGCCTGGGGCTTCAGTGAAGTTGTCCT 120

Qy        122 GCAAAGCTTCTGGCTACACATTCACTGATTATAGCTATACACTGGGTGAGACAGGCTCCT 181
              |||| |||||  |||||||| |||||    || ||| | |||||||  |||   ||||
Db        121 GCAAGGCTTCTGGCTACACCTTCACCAGCTACTATATGCACTGGGTGAAGCAGAGGCCTG 180

Qy        182 GACAGGGCCTCGAGTGGATTGGATTAATAATTTACTATGATAATACAAAATACAACGC 241
              |||| |||||  |||||||||| |  |||||  | | ||| |    || |||| |||
Db        181 GACAAGGCCTTGAGTGGATTGGGGGGATTAATCCTAGCAATGGTGGGACTAACTTCAATG 240

Qy        242 AGAAGTTTAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACATGC 301
              ||||||| ||| |||||||||||| |||||| |||| || | ||||||||||| |||
Db        241 AGAAGTTCAAGAGCAAGGCCACACTGACTGTGGACAAAATCCTCCAGCACAGCCTACATGC 300

Qy        302 AACTTAGTTCTTTGAGATCTGAGGATACGGCGGTTTATTACTGTGCAA  - -- GAG 352
              |||| ||     ||| |||||| || | || || ||||||||| ||| |  ||
Db        301 AACTCAGCAGCCTGACATCTGATGACTCTGCGGTCTATTACTGTACAAGGTTACTACGGG 360

Qy        353 CGGCCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
              | ||   | |||||||||||||||||||| |||   |||||||||||||||
Db        361 GGAACTATGGTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 413


RESULT 8
BF140551
LOCUS       BF140551                  771 bp    mRNA    linear   EST 24-OCT-2000
DEFINITION  601787584F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015172 5',
            mRNA sequence.
ACCESSION   BF140551
VERSION     BF140551.1  GI:10979591
KEYWORDS    EST
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   NIH MGC http://www.mgc.ncbi.nlm.nih.gov/
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9260  row: h  column: 21
            High quality sequence stop: 648.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="C3H/HeJ"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4015172"
                     /clone_lib="NCI_CGAP_Lu30"
                     /tissue_type="tumor, metastatic to mammary"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pCMV SPORT6; Site_1: NotI;
                     Site_2: SalI; transgenic model WNT 1, expression driven by
                     MMTV-LTR enhancer; Cloned unidirectionally.  Primer: oligo
                     dT.  Library constructed by Life Technologies.
                     Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT      179 a    215 c    195 g    182 t
ORIGIN

  Query Match             57.7%;  Score 233.8;  DB 12;  Length 771;
  Best Local Similarity   73.6%;  Pred. No. 1.5e-63;
  Matches  298;  Conservative    0;  Mismatches  107;  Indels    0;  Gaps    0;

Qy          1 AIAGGTTGGGAACTGTATCATCTTCTTTCTGGTTACCACACCTACACCCTCTGCACTTCCCAG 60
              |||| ||| ||| || | |||| || | |  | || |||||||| ||| | |||
Db         15 ATGGGATGGGGTGGGTCTTTCTCTTCCTCCTGTCAGTAACTGCAGGTGTCCACTCCCAG 74

Qy         61 GTCCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
              || ||| ||  |||||||||| |||||| ||  |||||||||| || |||||| ||||
Db         75 GTCCAGTTGAAGCAGTCTGGAGCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGCTGTCC 134

Qy        121 TGCAAAGCTTCTGGCTACACATTCACTGATTATAGCTATACACTGGGTGAGACAGGCTCCT 180
              |||| |||||  |||||||| |||    || ||| | |||||||  |||   ||||
Db        135 TGCAAGGCTTCTGGCTACACCTTCACCAGCTACTATATGCACTGGGTGAAGCAGAGGCCT 194

Qy        181 GGACAGGGCCTCGAGTGGATTGGATTAATAATTTACTATGATAATACAAACTACAAC 240
              |||||||||||  |||||||| |||    || |  ||| |||| |||| |||| |||
Db        195 GGACAAGGGCTTGAGTGGATTGGGGGGATTAATCCTAGCAATGGTGGGACTAACTTC 254

Qy        241 GAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAATCCTCCAGCACAGCCTACATG 300
              |||||||| |||||||||||| |||||| |||| || | ||||||||||| |||||
Db        255 GAAAAGTTCAAAGGCAAGGCCACACTGACTGTGGACAAAATCCTCCAGCACAGCCTACATG 314

Qy        301 GAACTTAGTTCTTTGAGATCTGAGGATACGGCGGTTTATTACTGTGCAAGAGGGGTTACTAC 360
              || || ||     ||| |||||| || | || || ||||||||| ||| |  ||||||||
Db        315 GAGCTCAGCAGCCTGACATCTGATGACTCTGCGGTCTATTACTGTGCAAGGGGTTACTAC 374

Qy        361 TATATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 405
              | |||||||||| |||| ||| | |||| ||||||||
Db        375 GTATTGGACTACTGGGGCAAGGCACCACTATCACAGTCTCCTCA 419


RESULT 9
BQ712275
LOCUS       BQ712275                  935 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  ACENO9001_B05450 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:6281117
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            5', mRNA sequence.
ACCESSION   BQ712275
VERSION     BQ712275.1  GI:21851174
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   NIH_MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLOYM2473  row: q  column: 06
            High quality sequence stop: 656.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo dT priming, directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT       201 a     302 c     252 g     173 t       7 others
ORIGIN

  Query Match             57.7%;  Score 233.8;  DB 14;  Length 935;
  Best Local Similarity   73.6%;  Pred. No. 1.6e-64;
  Matches  208;  Conservative    0;  Mismatches  107;  Indels    0;  Gaps    0;

Qy          1 AIGGGIIGGAACTGIAICAICIICIICCTGGIIACCACAGCIACAGGIGICACCCCAG 60
              |||| |||| ||| |   || |||| |||  |  |||||||||||| || ||||||
Db         44 AIGGACTGGACCTGGAGGCICCICTTTGTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAG 103

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
              |||||||||||||||||||||||||||||||||||||||||||||  ||| |||||| |||
Db        104 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCC 163

Qy        121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGCTCCT 180
              |||||  || ||  ||   |||  ||||      ||||||||  | ||||| |||||| |||
Db        164 TGCAAGGCCTCTGGAGGCACCTTCAGCAGCTATGCTATCAACTGGGTGCGACAGGCCCCT 223

Qy        181 GGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
              |||| || ||  |||||||| ||||  || |   |  || ||  |  |||||  |
Db        224 GGACAAGGGCTTGAGTGGATGGGAGGCATCATCCCTATCTTTGGAACGGCAAACTCTGCA 283

Qy        241 CAGAAGTTCAAGGGCAAGGCCACAATAACTGTAGACAAGTCGACGAGCACAGCCTATATG 300
              |||||||  ||||||  | ||||| || |  |||  |  ||  ||||||| | ||
Db        284 CAGAAGTTCCAGGGCAGAGTCACAATTACCGCGGACTCACAAACTGACACAGCCTTTTTG 343

Qy        301 GAACTTAGTCTCTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGGCGAGGCC 360
              ||  | ||     ||| |||||| || |||||||||||||||||| ||||  |
Db        344 GAGGTGAGCAGCCTGACATCTGACGACACGGCCGTTTATTACTGTGCGAGAGGCGAGGCC 403

Qy        361 TATATCGACTACTGGGGCCAAGGTACCCTGGTCACCGTCTCCTCA 405
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Db        404 TACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA 448
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RESULT 10
BQ709671
LOCUS       BQ709671                 949 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8254825 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278491
            5', mRNA sequence.
ACCESSION   BQ709671
VERSION     BQ709671.1  GI:21848520
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 949)
  AUTHORS   NIH_MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLOYM2469  row: i  column: 20
            High quality sequence stop: 618.
FEATURES             Location/Qualifiers
     source          1..949
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6278491"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo dT priming, directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT       206 a     315 c     250 g     177 t       1 others
ORIGIN

  Query Match             57.7%;  Score 233.8;  DB 14;  Length 949;
  Best Local Similarity   73.6%;  Pred. No. 1.6e-64;
  Matches  209;  Conservative    0;  Mismatches  107;  Indels    0;  Gaps    0;

Qy          1 AIGGGIIGGAACTGIAICAICIICIICCTGGIIACCACAGCIACAGGIGICACCCCAG 60
              |||| |||| ||| |   || |||| |||  |  |||||||||||| || ||||||
Db         45 AIGGACTGGACCTGGAGGCICCICTTTGTGGTGGCAGCAGCTACAGGTGTCCAGTCCCAG 104

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
              |||||||||||||||||||||||||||||||||||||||||||||  ||| |||||| |||
Db        105 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCTCC 164

Qy        121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGCTCCT 180
              |||||  || ||  ||   |||  ||||      ||||||||  | ||||| |||||| |||
Db        165 TGCAAGGCCTCTGGAGGCACCTTCAGCAGCTATGCTATCAACTGGGTGCGACAGGCCCCT 224

Qy        181 GGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
              |||| || ||  |||||||| ||||  || |   |  || ||  |  |||||  |
Db        225 GGACAAGGGCTTGAGTGGATGGGAGGCATCATCCCTATCTTTGGAACGGCAAACTCTGCA 284

Qy        241 CAGAAGTTCAAGGGCAAGGCCACAATAACTGTAGACAAGTCGACGAGCACAGCCTATATG 300
              |||||||  ||||||  | ||||| || |  |||  |  ||  ||||||| | ||
Db        285 CAGAAGTTCCAGGGCAGAGTCACAATTACCGCGGACTCACAAACTGACACAGCCTTTTTG 344

Qy        301 GAACTTAGTCTCTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGGCGAGGCC 360
              ||  | ||     ||| |||||| || |||||||||||||||||| ||||  |
Db        345 GAGGTGAGCAGCCTGACATCTGACGACACGGCCGTTTATTACTGTGCGAGAGGCGAGGCC 404
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Qy          361 TATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
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Db          405 TACTTTGACTACTGGGGCCAAGGAACCGTGGTCACCGTCTCCTCA 449


RESULT 11
BQ952037
LOCUS       BQ952037                 863 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_8952454 NCI_CGAP_Co24 Mus musculus cDNA clone
            IMAGE:6477061 5', mRNA sequence.
ACCESSION   BQ952037
VERSION     BQ952037.1  GI:22367515
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 863)
  AUTHORS   NIH-MGC http://mgc.nih.gov/
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14018  row: q  column: 14
            High quality sequence stop: 693.
FEATURES             Location/Qualifiers
     source          1..863
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6477061"
                     /clone_lib="NCI_CGAP_Co24"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Strain: FVB/N; Vector: pCMV-SPORT6; Site_1:
                     Site_2: Sall; Cloned unidirectionally.  Primer: oligo dT.
                     Average insert size 1.6 kb.  Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      206 a    250 c    209 g    195 t      3 others
ORIGIN

  Query Match          57.1%;  Score 232.6;  DB 14;  Length 863;
  Best Local Similarity   74.6%;  Pred. No. 3.8e-64;
  Matches  311;  Conservative    0;  Mismatches   94;  Indels   12;  Gaps    1;

Qy          1 ATGGCTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
              ||||| |||| |||||||||| ||||| |||| | ||||||||||||  ||||||||||
Db         36 ATGGGATGGAGCTGTATCATCCTCTTTTTGGTAGCAACAGCTACAGGTGGCCACTCCCAG 95

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTGTCC 120
              ||||| ||| |||| |||||||||| |   |||||||||   |||||||  |||||
Db         96 GTCCAACTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAAAATGTCC 155

Qy        121 TGCAAAGCTTCTGGCTACACCTTCACCAGCTACTGGATAAACTGGGTGAAGCAGAGGCCT 180
              ||||| ||||| |||||||| ||||    ||    ||| | |||||||| |||   |||
Db        156 TGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATAAACTGGGTGAAGCAGAGGCCT 215

Qy        181 GGACAGGGCCTCGAGTGGATTGGAGATATTTATCCTGGTAGAGGTATGACTAACTACAAC 240
              ||||| ||||| |||||||||||| ||| ||  |     | ||  || ||||||||
Db        216 GGACAAGGCCTTGAGTGGATTGGAGATATTTATCCTGGTAGAGGTATGACTAACTACAAC 275

Qy        241 GAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAGTCGAGCAGCACAGCCTACATG 300
              | ||||| |||  |||||||||| |||| |||||   |  | ||||||||||| |||
Db        276 GACAAGTTCAAGAGCAAGGCCACACTGACTGTAGACACAACCTCCAGCACAGCCTACATG 335

Qy        301 GAACTTAGCTCCTTGAGATCTGAGGATACGGCCGTCTATTACTGTGCAAGAGGG------ 354
                                                                  ||||||
Db        336 CAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGTCAAGAGGGGAAGT 395

Qy        355 ------GGCTGGTATATGGACTACTGGGGTCAAGGAACCTTGTCACCGTCTCCTCA 405
                    |||| |||||||||||||||||||||| |||  ||||||||||||||||
Db        396 AACTACGGCTTTGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 452


RESULT 12
BQ969577
LOCUS       BQ969577                 723 bp    mRNA    linear   EST 12-JUN-2001
DEFINITION  602037486F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4971814
            5', mRNA sequence.
ACCESSION   BQ969577
VERSION     BQ969577.1  GI:14357214
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 723)
  AUTHORS   NIH-MGC http://mgc.nih.gov/
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, LLC.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10957  row: l  column: 22
            High quality sequence stop: 723.
FEATURES             Location/Qualifiers
     source          1..723
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4971814"
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: oligo dT.
                     Average insert size 1.75 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      179 a    196 c    193 g    155 t
ORIGIN

  Query Match          57.3%;  Score 232;  DB 14;  Length 723;
  Best Local Similarity   74.8%;  Pred. No. 5.3e-63;
  Matches  305;  Conservative    0;  Mismatches  100;  Indels    3;  Gaps    1;

Qy          1 ATGGCTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
              ||||| |||| |||||||||| ||||| |||| | ||||||||||||  ||||||||||
Db         36 ATGGGATGGAGCTGTATCATCCTCTTTTTGGTAGCAACAGCTACAGGTGGCCACTCCCAG 95

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTGTCC 120
              ||||| ||| |||| |||||||||| |   |||||||||   |||||||  |||||
Db         96 GTCCAACTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAAAATGTCC 155

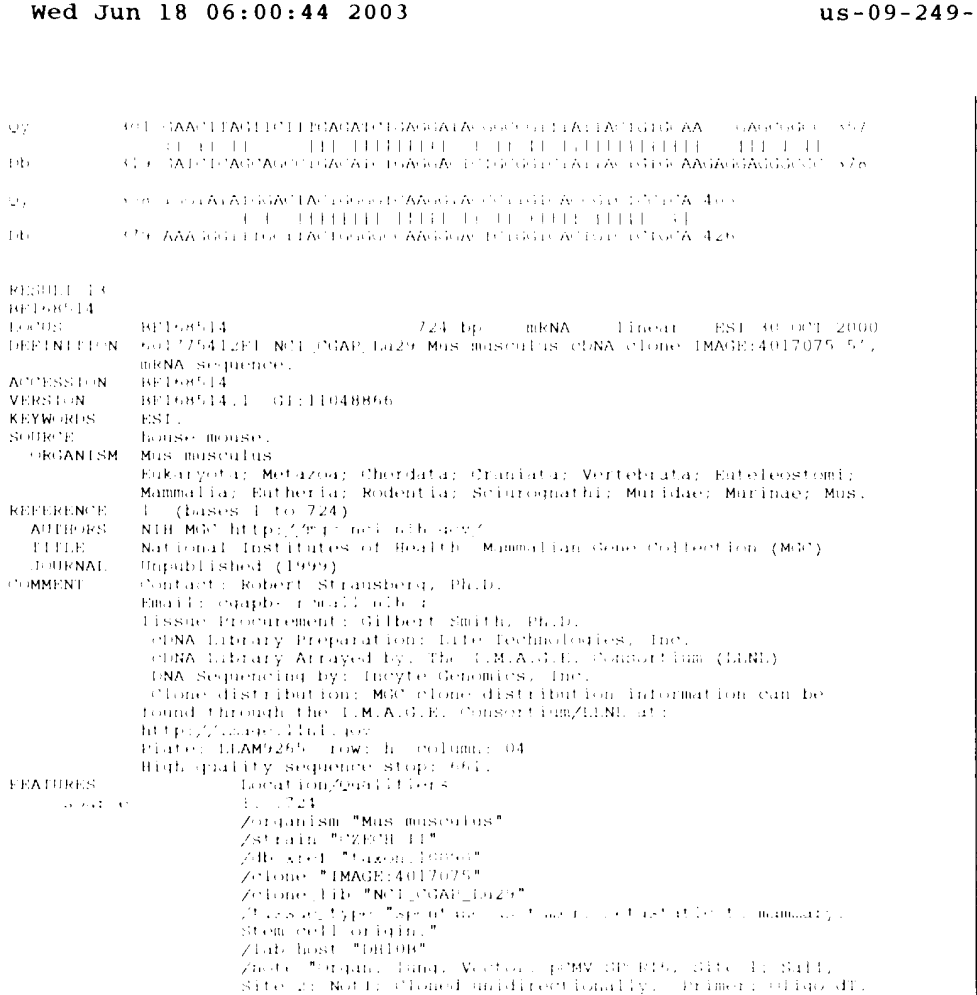
Qy        121 TGCAAAGCTTCTGGCTACACCTTCACCAGCTACTGGATAAACTGGGTGAAGCAGAGGCCT 180
              ||||| ||||| |||||||| ||||    ||    ||| | |||||||| |||   |||
Db        156 TGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATAAACTGGGTGAAGCAGAGGCCT 215

Qy        181 GGACAGGGCCTCGAGTGGATTGGAGATATTTATCCTGGTAGAGGTATGACTAACTACAAC 240
              ||||| ||||| |||||||||||| ||| ||  |     | ||  || ||||||||
Db        216 GGACAAGGCCTTGAGTGGATTGGAGATATTTATCCTGGTAGAGGTATGACTAACTACAAC 275

Qy        241 GAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAGTCGAGCAGCACAGCCTACATG 300
              | ||||| |||  |||||||||| |||| |||||   |  | ||||||||||| |||
Db        276 GACAAGTTCAAGAGCAAGGCCACACTGACTGTAGACACAACCTCCAGCACAGCCTACATG 335

Qy        301 GAACTTAGCTCCTTGAGATCTGAGGATACGGCCGTCTATTACTGTGCAAGAGGG------ 354
                                                                  ||||||
Db        336 CAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGTCAAGAGGGGAAGT 395

Qy        355 ------GGCTGGTATATGGACTACTGGGGTCAAGGAACCTTGTCACCGTCTCCTCA 405
                    |||| |||||||||||||||||||||| |||  ||||||||||||||||
Db        396 AACTACGGCTTTGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 452
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RESULT 13
BF106514
LOCUS BF106514 724 bp mRNA linear EST 30-OCT-2000
DEFINITION 601775412F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017075 5', mRNA sequence.
ACCESSION BF106514
VERSION BF106514.1 GI:11048866
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 724)
AUTHORS NIH_MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9269 row: h column: 04
High quality sequence stop: 661.
FEATURES Location/Qualifiers
source 1..724
/organism="Mus musculus"
/strain="ZEN II"
/db_xref="taxon:10090"
/clone="IMAGE:4017075"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spleen"
/lab_host="DH10B"
/note="Organ: fetal; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally; Primer: oligo dT; Library constructed by Life Technologies; Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 185 a 186 c 194 g 159 t
ORIGIN

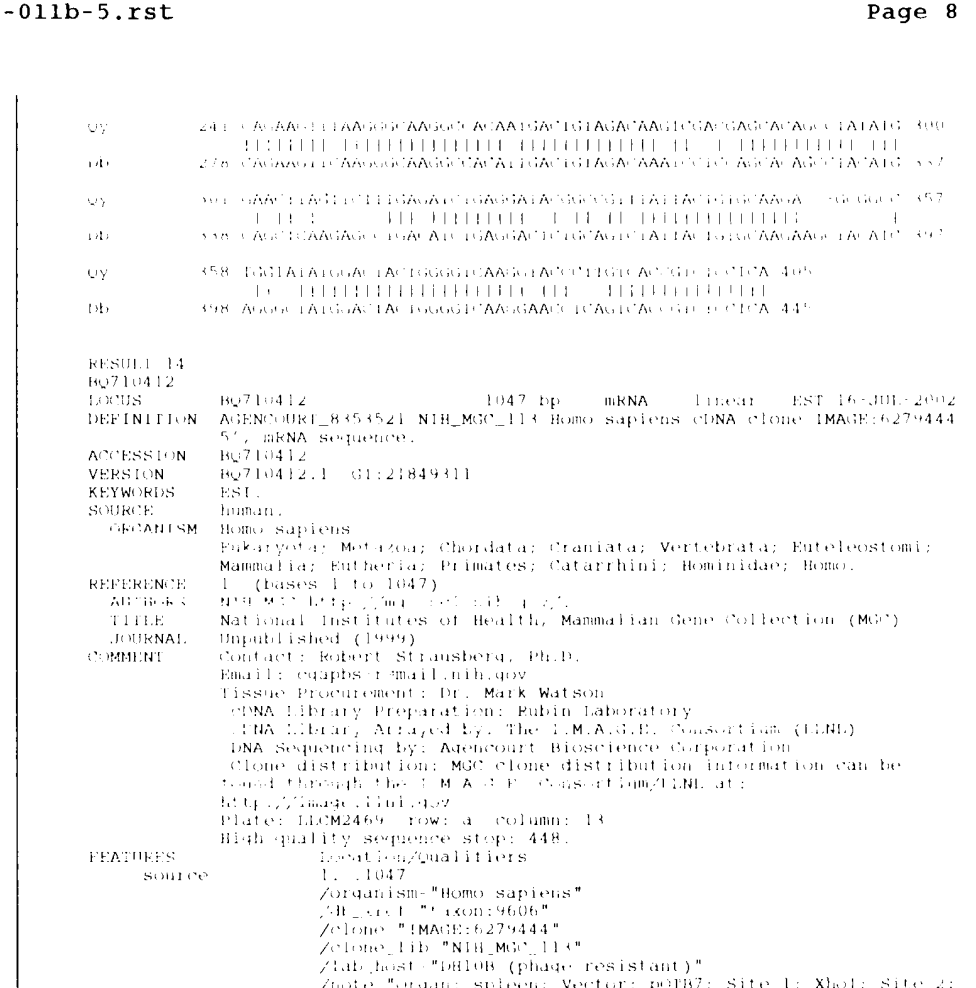
Query Match 57.4%; Score 232; DB 12; Length 724;
Best Local Similarity 74.8%; Pred. No. 5.3e-63;
Matches 306; Conservative 0; Mismatches 103; Indels 3; Gaps 1;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
Db 98 ATGGGATGGAGCTGGATCTTTATTTTAATCTGTCAGTAACTACAGGTGTCCACTCTGAG 97

Qy 61 GTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCC 120
Db 98 GTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGCATATCC 157

Qy 121 TGCAAAGCTTCCTGGCTACACATTCACTGATTATGTTATAAACTGGGTGAAGCAGAGGCCTGGA 180
Db 158 TGCAAGGCTTCTGGTTACACATTCACTGACTACTATATAAACTGGGTGAAGCAGAGGCCTGGA 217

Qy 181 CAAGGCCTTGAGTGGATTGGAGAGATTAATCCTAATAATGATGATACTAACTACAAC 240
Db 218 CAAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCC 277



RESULT 14
BQ710412
LOCUS BQ710412 1047 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8353521 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279444 5', mRNA sequence.
ACCESSION BQ710412
VERSION BQ710412.1 GI:21849311
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1047)
AUTHORS NIH_MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2469 row: a column: 13
High quality sequence stop: 448.
FEATURES Location/Qualifiers
source 1..1047
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/db_xref="taxon:9606"
/clone="IMAGE:6279444"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage resistant)"
/note="Organ: spleen; Vector: pCMV7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adapter: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 209 a 473 c 257 g 208 t
ORIGIN

Query Match 56.9%; Score 230.6; DB 14; Length 1047;
Best Local Similarity 74.5%; Pred. No. 1.8e-62;
Matches 306; Conservative 0; Mismatches 99; Indels 6; Gaps 1;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
Db 98 ATGGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGCAGCTACAAGTGCCACTCCCAG 97

Qy 61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 120
Db 98 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 157

Qy 121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGTTATAAACTGGGTGAAGCAGGCCCCTGGA 180
Db 158 TGCAAGGCTTCTGGTTACACCTTTACCGGCTACTATATGCACTGGGTGCGACAGGCCCCTGGA 217

Qy 181 CAAGGGCTTGAGTGGATGGGATGGATCAACCCTAACAGTGGTGGCACAAACTATGCACAG 240
Db 218 CAAGGGCTTGAGTGGATGGGACGGATCAACCCTAACAGTGGTGGCACAAACTATGCACAG 277

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Db        158 TGTAAGGCTTCTGGATACACTTCACCAGTTATGATATCAACTGGGTGCGACAGGCCACT 217

Qy        181 GGACAGGGCCTCGAGTGGATTGGATGGATAATTAACTATGATAACCCAAACTACAAC 240
              ||||| || || |||||||| |||  || ||  | ||  || ||| |||  |||
Db        218 GGACAAGGGCTTGAGTGGATGGGATGGATGAACCCTAACAGTGGTAACACAGCTATGCA 277

Qy        241 CAGAAGTTTAAGGGCAAGGCCACACTGACTGTAGACAACTCCGACGAGCACAGCCTAGCA 300
              |||||||  |||||  | ||| ||||     ||| || | ||||||||||| |||
Db        278 CAGAAGTTCCAGGGCAGAGTCACCATGACCAGGAACACCTCCATAAGCACAGCCTACATG 337

Qy        301 GAACTTAGTTCTTTGACATCTGAGGATACGGCCGTTTATTACTGTGCTAAGGAG      356
              || || ||     ||||||||||||| ||||||| ||||||||||| |||
Db        338 GAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGGGAGAGGCTACGA 397

Qy        357 GTCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 406
                 ||       ||| |||||||||| || || || || ||||||||||||||||
Db        398 TCCCCCGGACTGGGCTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA 447


RESULT 15
BF168856
LOCUS       BF168856                 769 bp    mRNA    linear   EST 30-OCT-2000
DEFINITION  601775314F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017147 5',
            mRNA sequence.
ACCESSION   BF168856
VERSION     BF168856.1  GI:11049208
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 769)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9265  row: k  column: 04
            High quality sequence stop: 678.
FEATURES             Location/Qualifiers
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                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4017147"
                     /clone_lib "NCI_CGAP_Lu29"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host "DH10B"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
BASE COUNT      190 a    226 c    189 g    164 t
ORIGIN

  Query Match           56.9%;  Score 230.4;  DB 12;  Length 769;
  Best Local Similarity   74.5%;  Pred. No. 1.8e-62;
  Matches  304;  Conservative    0;  Mismatches  101;  Indels    3;  Gaps    1;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACTACAGCTACAGGTGTGCACTCCCAG 60
              ||||| |||| ||| ||| |  | ||  |  |  |  |  | ||||||||| |||||  ||
Db         42 ATGGGATGGAGCTGGATCTTTATTTTAATCCTGTCAGTAACTACAGGTGTCCACTCTGAG 101

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 120
              ||||||||  ||||||||  ||||| ||  |||||||||   |||||||| | |||

Db        102 GTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCC 161

Qy        121 TGTAAGGCTTCTGGATACACATTCACTGACTACTATATAAACTGGGTGAAGCAGAGCCATG 180
              ||||| |||| || ||| ||||||||  ||     || |  |||||||  ||  ||||
Db        162 TGTAAGGCATCTGGATTCACTTTC ACTAGCTACTATATGCACTGGGTGAAGCAAAGGCCT 221

Qy        181 GGACAGGGCCTCGAGTGGATTGGATGGATAATTAACTATGATAACCCAAACTACAACCAG 240
              | | || |||| ||||||||||||  ||||||  |  |  || |  |||||||  ||  ||||
Db        222 GAAAAGAGCCTTGAGTGGATTGGAGAGATTAATCCTAGCAATGGTGGTACTAACTACAAC 281

Qy        241 AAGAAGTTCAAGAGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 300
              |||||||| ||||||||||||||| ||||||||  | |  | ||||||||||| |||
Db        282 GAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 341

Qy'       301 GAACTTAGTTCTTTGACATCTGAGGATACGGCCGTTTATTACTGTGCTAAGGA  GCGGCT 357
              | || |      ||| |||||'|||  | || || ||||||||||||||||        |
Db        342 CAACTCAACAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGAAGCTACTAT 401

Qy        358 TGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
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Db        402 AGGGCTATGGACTACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCA 449


Search completed: June 17, 2003, 19:59:15
Job time : 1845.87 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 13:02:29 ; Search Time 54.343 Seconds
(without alignments)
5639.472 Million cell updates/sec

Title: US-09-249-011B-5
Perfect score: 405
Sequence: 1 atgaattggaactgtatcat.....ccctttatcaccgtatcctca 405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 447c478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	405	100.0	405	21	AAA59694	DNA encoding heavy
2	384.6	82.6	405	21	AAA59692	Nucleotide sequence
3	277.2	68.4	524	12	AAQ14802	Encodes murine ant
4	277.2	68.4	524	12	AAQ14652	Rc-5-D6 anti-ICAM
5	272.2	67.2	446	11	AAQ05554	Sequence encoding
6	265.8	65.6	1767	19	AAV61363	Anti-human Fas hum
7	265.8	65.6	1767	21	AAA78271	Anti human Fas imm
8	265.8	65.6	1768	19	AAV61364	Anti human Fas hum
9	265.8	65.6	1768	21	AAA78272	Anti-human Fas imm
10	254.4	62.8	424	17	AAI42717	BuMo1 VH coding se
11	253.6	62.6	451	15	AAQ66782	HKPC 200 Humanised
12	253.6	62.6	2071	19	AAV20888	Anti Fas humanised
13	253.6	62.6	2071	21	AAA72184	DNA encoding human
14	253.6	62.6	2071	21	AAA11622	Humanised BE2/A he
15	253.6	62.6	2071	24	ABL46001	Humanised anti Fas
16	253.6	62.6	2071	24	ABL48744	Humanised anti Fas
17	253	62.5	4250	24	AAR26268	Cytomegalovirus (C
18	253	62.5	4250	24	AAD28307	Cytomegalovirus (C
19	252	62.2	2073	21	AAA11644	Humanised anti Fas
20	252	62.2	2073	21	AAA11645	Humanised anti Fas
21	252	62.2	2073	24	ABL46023	Humanised anti Fas
22	252	62.2	2073	24	ABL46024	Humanised anti Fas
23	251.6	62.1	423	21	AAB00905	Humanised antibody
24	250.4	61.8	2073	21	AAA11646	Humanised anti Fas
25	250.4	61.8	2073	24	ABL46025	Humanised anti Fas
26	248.8	61.4	457	19	AAV20104	Anti Fas humanised
27	248.8	61.4	457	21	AAA72116	Humanised anti Fas
28	248.8	61.4	457	21	AAA11584	Humanised anti Fas
29	248.8	61.4	457	24	ABL45963	Humanised anti Fas
30	248.8	61.4	457	24	ABL48706	Humanised anti Fas
31	248.8	61.4	2077	19	AAV20379	Anti Fas humanised
32	248.8	61.4	2077	21	AAA72159	DNA encoding human
33	248.8	61.4	2077	21	AAA11597	Humanised BE2/A he
34	248.8	61.4	2077	24	ABL45976	Humanised anti Fas
35	248.8	61.4	2077	24	ABL48719	Humanised anti Fas
36	248.2	61.3	405	21	AAA59698	DNA encoding heavy
37	247.6	60.6	2077	21	AAA11655	Humanised anti Fas
38	245.6	60.6	2077	24	ABL48751	Humanised anti Fas
39	245.2	60.5	423	21	AAB00907	Humanised antibody
40	245	60.5	405	20	AAV33047	Anti CD33 antibody
41	245	60.5	405	22	AAF58738	Murine M195 antibo
42	245	60.5	451	21	AAA19645	cDNA encoding huma
43	243.6	60.1	424	22	AAB77568	Anti-CD33 Fab VH F
44	243.6	60.1	424	22	AAB77617	Anti human FIt 1 a
45	243.4	60.1	405	19	AAV37264	cDNA encoding a hu

ALIGNMENTS

RESULT 1
AAA59694
ID AAA59694 standard; DNA; 405 BP.
XX
AC AAA59694;
XX
DT 31-DEC-1990 (first entry)
XX
DE DNA encoding the heavy chain variable region of humanized anti-antibody.
XX
KW Ab-Ag complex; humanized immunoglobulin.
KW for therapeutic intervention in autoimmune disease or inflammatory disorder;
KW systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome; ss.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FH Key Location/qualifiers
FT CDS 1..405
FT /label= a
FT /product= "heavy chain variable region of sFas antibody"
FT /note= "no termination codon given."
FT sig_peptide 1..57
FT /label= b
FT mat_peptide 58..405
FT /label= c
XX

PN WO200047625 A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US03403.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMY) GENELTECS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524542/47.
DR P-PSDB; AAB07963.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases
XX
PS Example 1; Fig 1A; 162pp; English.
XX
CC The present sequence encodes the heavy chain variable region of the
CC humanised murine antibody 4D1. The antibody has a binding specificity to
CC B7 molecules. The antibody is used to construct humanized
CC immunoglobulins, which comprise an antigen binding region of non human
CC origin and a portion of a human immunoglobulin. The humanized
CC immunoglobulins are useful for treating autoimmune diseases, infectious
CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 405 BP; 102 A; 88 C; 110 G; 105 T; 0 other;

Query Match 100.0%; Score 405; DB 21; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.9e-101;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTAGCAACAGCTACAGGTGTGCACTCCCAG 60
Db 1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTAGCAACAGCTACAGGTGTGCACTCCCAG 60

Qy 61 GTCCAGCTGCAGCAGTCTGGGGCTGAGCTGGAAGAACCTGGGGCCTCAGTGAAGGTGTCC 120
Db 61 GTCCAGCTGCAGCAGTCTGGGGCTGAGCTGGAAGAACCTGGGGCCTCAGTGAAGGTGTCC 120

Qy 121 TGCAAAGCTTCTGGCTACACCTTCACTAGCTATGTTATAAGCTGGGTGAGACAGGCCCCT 180
Db 121 TGCAAAGCTTCTGGCTACACCTTCACTAGCTATGTTATAAGCTGGGTGAGACAGGCCCCT 180

Qy 181 GGACAAGGGCTTGAGTGGATGGGATGGATTAATGCTTACAATGGTAACACAAACTATGCA 240
Db 181 GGACAAGGGCTTGAGTGGATGGGATGGATTAATGCTTACAATGGTAACACAAACTATGCA 240

Qy 241 CAGAAGTTTCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGCCTACATG 300
Db 241 CAGAAGTTTCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGCCTACATG 300

Qy 301 GAACTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGCGGGCCTGG 360
Db 301 GAACTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGCGGGCCTGG 360

Qy 361 TATAGCGACTACGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
Db 361 TATAGCGACTACGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405

RESULT 2
AAA59692
ID AAA59692 standard; DNA; 405 BP.
XX
AC AAA59692;
XX
DT 14-NOV-2000 (first entry)
XX
DE Nucleotide sequence of heavy chain variable region of 4D1 antibody.
XX
KW Antibody 4D1; B7 molecule; B7; humanised immunoglobulin;
KW autoimmune disease; infectious disease; inflammatory disorder;
KW systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..405
FT /*tag= a
FT /product= "heavy chain variable region of 4D1 antibody"
FT /note= "no termination codon given"
FT sig_peptide 1..57
FT /*tag= b
FT mat_peptide 58..405
FT /*tag= c
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PN WO200047625 A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US03403.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMY) GENELTECS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524542/47.
DR P-PSDB; AAB07963.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases
XX
PS Example 1; Fig 1A; 162pp; English.
XX
CC The present sequence encodes the heavy chain variable region of the
CC murine antibody 4D1. The antibody has a binding specificity to B7
CC molecules. The antibody is used to construct humanized immunoglobulins,
CC which comprise an antigen binding region of non human origin and a
CC portion of a human immunoglobulin. The humanized immunoglobulins are
CC useful for treating autoimmune diseases, infectious diseases,
CC inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 405 BP; 110 A; 89 C; 102 G; 104 T; 0 other;

Query Match 82.0%; Score 334.6; DB 21; Length 405;

Best Local Similarity 87.1%, Pred. No. 2.7e-62,
Matches 467; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

RESULT 3
AAQ14802
ID AAQ14802 standard; DNA; 524 BP.
XX
AC AAQ14802;
XX
DT 14-FEB-1992 (first entry)
XX
DE Encodes murine anti-ICAM monoclonal antibody heavy chain.
XX
KW Intercellular adhesion molecule; variable region, V(H), mouse,
KW K6.5.E6 murine MAb; complementarity determining region; CDR; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT sig_peptide 34..90
FT /*tag= a
FT /standard_name= leader
FT CDS 34..524
FT /*tag= b
XX
PN WO9119927-A.
XX
PD 12-DEC-1991.
XX
PF 29-APR-1991; 91WO-US02942.
XX
PR 27-APR-1990; 90GB-0009549.
XX
PA (CELL) CELLTECH LTD.
PA (BOEH) BOEHRINGER INGELHEIM PHA.
XX
PI Adair JR, Athwal DS, Rothlein RA;
XX
DR WPI; 1992-056533/48.
DR P-PSDB; AAK15060.
XX
PT New humanised CDR-grafted anti-ICAM antibodies - used to treat
PT and prevent inflammation (e.g. psoriasis) tumours, viral
PT infections and asthma and in diagnosis
XX
PS Disclosure; Fig 2; 85pp; English.
XX
CC The heavy chain sequence was isolated from a cDNA library prepd. from
CC hybridoma cell line K6.5.E6 which secretes murine IgG2a/kappa
CC antibody. The library was screened using a 930bp BamHI EcoRI
CC fragment of a previously isolated mouse IgG2a constant region
CC clone. The murine framework encoding sequences (i.e. not encoding
CC CDRs) will be replaced by human framework sequences to produce
CC recombinant (CDR grafted humanised) antibody molecules having
CC specificity for ICAM 1.
XX
SQ Sequence 524 BP; 128 A; 130 C; 135 G; 131 T; 0 other;

Query Match 88.4%; Score 277.2; DB 12; Length 524;
Best Local Similarity 81.4%; Pred. No. 1.8e-66;
Matches 367; Conservative 0; Mismatches 58; Indels 9; Gaps 1;

RESULT 4
AAQ14652
ID AAQ14652 standard; cDNA; 524 BP.
XX
AC AAQ14652;
XX
DT 14-FEB-1992 (first entry)
XX
DE 29-5.19 anti-ICAM 1 heavy chain.
XX
KW Intercellular adhesion molecule1; antibody; chimaeric; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT sig_peptide 34..90
FT /*tag= a
FT CDS 91..524
FT /*tag= b
XX
PN WO9119028-A.
XX
PD 12-DEC-1991.
XX
PF 29-APR-1991; 91WO-US02646.
XX

```
RESULT 5
AAQ05554
ID   AAQ05554 standard; DNA; 446 BP.
XX
AC   AAQ05554;
XX
DT   10-DEC-1990  (first entry)
XX
DE   Sequence encoding variable region of murine AHI 107 heavy chain.
XX
KW   Interleukin 2 receptor; IL-2; tumour necrosis factor; TNF; ss:
XX
OS   Mus sp.
XX
FH   Key             Location/qualifiers
FT   CDS             45..446
FT                   /*tag= a
XX
PN   EP380068-A.
XX
PD   01-AUG-1990.
XX
PF   24-JAN-1990;    90EP-0101451.
XX
PR   04-DEC-1989;    89US-0441702.
PR   24-JAN-1989;    89US-0301216.
XX
PA   (MOLE-) MOLECULAR THERAPEU.
XX
PI   Zeiler B;
XX
DR   WPI; 1990-252892/31.
DR   P-PSDB; AAR08250.
XX
PT   Expression vectors for producing chimeric monoclonal antibodies -
PT   which express human constant region and non-human variable region
XX
PS   Disclosure; ; pp; English.
XX
CC   MAbs comprising mouse CH and CL constant regions whith human
CC   variable regions may be used to create mouse/human hybrid MAbs,
CC   which have a longer serum half-life. Method can be used to produce
CC   Abs against interleukin-2 receptor and tumour necrosis factor.
XX
SQ   Sequence 446 BP; 117 A; 110 C; 113 G; 106 T; 0 other;

  Query Match             67.2%;  Score 297.2;  DB 11;  Length 446;
  Best Local Similarity   81.2%;  Pred. No. 4.1e-65;
  Matches  522;  Conservative    0;  Mismatches   74;  Indels    4;  Gaps    1;
```

```
Qy          961 [ATATCGACTACTGGGGTCAAGGTACCCTGGTCACCGTCTCCTCA 405
                |||||||||||||||||||||||||||||||||||||||||||||
Db          402 AACCTTGACTACTGGGGCCAAGGCACCCTCGTCACCGTCTCCTCA 446


RESULT 6
AAV61866
ID   AAV61866 standard; cDNA to mRNA; 1767 BP.
XX
AC   AAV61866;
XX
DT   18-JAN-1999  (first entry)
XX
DE   Anti human Fas humanised antibody CH11 heavy chain hmuH cDNA.
XX
KW   Recombinant protein; Fas; CH11; monoclonal antibody; ss;
KW   anti-immune disease; rheumatoid arthritis; therapy; human;
KW   antibody engineering; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     1..57
FT                   /*tag= a
FT   mat_peptide     58..1764
FT                   /*tag= b
XX
PN   EP899341-A2.
XX
PD   24-SEP-1998.
XX
PF   20-MAR-1998;    98EP-0302113.
XX
PR   21-MAR-1997;    97JP-0067938.
XX
PA   (SANY ) SANKYO CO LTD.
XX
IN   Kamiguchi H; Nakamura K; Yoshizawa N; Takahashi T;
IN   Yamamura S;
XX
DR   WPI; 1998-487205/42.
DR   P-PSDB; AAW71880.
XX
PT   Production of anti Fas protein humanised antibodies - for use in
PT   inducing apoptosis on Fas expressing cells in the treatment of
PT   anti-immune diseases, especially rheumatoid arthritis
XX
PS   Example 3; Page 103-105; 187pp; English.
XX
CC   This cDNA sequence codes for a humanised anti-Fas antibody CH11
CC   heavy chain (see AAW71880), designated hmuH. hmuH is based on the
CC   light chain (see AAW71878) of murine anti human Fas monoclonal
CC   antibody CH11. The humanised sequence was designed following
CC   selection of donor residues from CH11 to be grafted onto acceptor
CC   molecule 21.28'2'1. 2 light chain sequences (see AAW71880-81) have
CC   been designed, and each can be used in combination with any of 4
CC   light chain sequences (see AAW71876-77) to provide novel, claimed
CC   humanised CH11 IgM antibodies that lack a J chain. These humanised
CC   anti-human Fas antibodies are capable of inducing apoptosis in cells
CC   expressing Fas (e.g. synoviocytes) and are useful in the treatment
CC   of autoimmune disease and chronic rheumatoid arthritis. DNA
CC   sequences encoding the humanised antibodies are claimed, as are
CC   vectors such as pHmuH5-1 including the HmuH nucleotide sequence,
CC   and host cells such as Escherichia coli pHmuH5-1 (FERM BP-5865).
XX
SQ   Sequence 1767 BP; 384 A; 568 C; 485 G; 330 T; 0 other;

  Query Match           65.6%;  Score 265.8;  DB 19;  Length 1767;
  Best Local Similarity   78.5%;  Pred. No. 3.4e-63;
  Matches  318;  Conservative    0;  Mismatches   87;  Indels    0;  Gaps    0;

Qy            1 AVQGGTGGAACTGTACATCTACTTCTGGTTACCAGCTACAGGTGTCCACTCTCAG 60
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 ATGAGATGGAGCTGGATCTTTCTCTTCCTCCTGTCAGGAACTGCAGGTGTCCACTCTGAG 60

Qy           61 GTCCAGCTGCAACAGTCTGGACCTGAGCTGGAGAAGCCTGGCGCTTCAGTGAAGATATCCTGC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 GTGCAGCTTCAGCAGTCTGGGACTGAGCTGGCAAAACCTGGGGCCTCAGTGAAGATGTCCTGC 120

Qy          121 AAGGCTTCTGGCTACACATTCACTAGATACACTATACACTGGGTGAAACAGAGGCCTGGA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 AAGGCTTCTGGCTACACATTCACTAGATACACTATACACTGGGTGAAACAGAGGCCTGGA 180

Qy          181 CAGGGCCTTGAATGGATTGGATACATTAATCCTAGCAGAGGTTATACTAATTACAATCAGAAG 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 CAGGGCCTTGAATGGATTGGATACATTAATCCTAGCAGAGGTTATACTAATTACAATCAGAAG 240

Qy          241 TTCAAGGACAAGGCCACATTGACTACAGACAAATCCTCCAGCACAGCCTACATGCAACTGAGC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 TTCAAGGACAAGGCCACATTGACTACAGACAAATCCTCCAGCACAGCCTACATGCAACTGAGC 300

Qy          301 GACCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGGGCCTCGG 354
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 GACCTGACGTCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGGGCCTCGG 354

Qy          355 TATATCGACTACTGGGGTCAAGGTACCCTGGTCACCGTCTCCTCA 405
                |||||||||||||||||||||||||||||||||||||||||||||
Db          355 GTTATCGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA 405


RESULT 7
AAA78271
ID   AAA78271 standard; DNA; 1767 BP.
XX
AC   AAA78271;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Anti human Fas immunoglobulin M heavy chain DNA sequence SEQ ID #85.
XX
KW   Antibody-mediated lysis; immunoglobulin M; IgM; apoptosis inducer;
KW   immunosuppression; autoimmune disease; treatment; rheumatism;
KW   anti Fas antibody; ss.
XX
OS   Synthetic.
XX
PN   JP2000154149-A.
XX
PD   06-JUN-2000.
XX
PF   17-SEP-1999;    99JP-0263984.
XX
PR   18-SEP-1998;    98JP-0264508.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2000-454476/40.
DR   P-PSDB; AAG12017.
XX
PI   Anti human Fas humanizing antibody-containing antirheumatic agents
XX
PS   Example 2; Page 75-76; 109pp; Japanese.
XX
CC   The present invention relates to antirheumatic agents which comprise as
CC   active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC   does not include a J segment, has apoptosis inducing activity, and
CC   consists of a light and heavy chain polypeptide produced synthetically.
CC   The agents of the invention exhibit antirheumatic and immunosuppressive
CC   activity and can be used to treat autoimmune diseases, especially
CC   rheumatism. The IgM molecule used in the invention has human Fas antibody
CC   binding properties. Included in the invention are nucleotide sequences
CC   of the IgM light and heavy chains (see AAA78267-AAA78272) and the
CC   corresponding protein sequences (see AAA12015-AAA12018 and AAG12019) and
CC   nucleotide sequences of the humanised anti human Fas Ig CH11 (see
```

CC AAA78202 A78276) and protein sequences (see AAB12908 B12910). Also
CC included are anti human Fas antibody CDP peptides (AAB12902-B12907).
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC chains used in the invention are represented by sequences
CC AAA78214 A78226. Primers used for sequencing the human Ig DNA used in the
CC invention are represented by sequences AAA78277 A78318 and
CC AAA78305 A78337, while humanised anti Fas Ig DNA sequencing primers are
CC represented by sequences AAA78321 A78334 and AAA78338 A78367. Primer
CC sequences AAA78207 A78212 are specific for murine Ig DNA, and are used in
CC the production of the agent of the invention.
XX
SQ Sequence 1767 BP; 384 A; 568 C; 485 G; 330 T; 0 other;

Query Match 65.6%; Score 265.8; DB 21; Length 1767;
Best Local Similarity 78.5%; Pred. No. 4.4e-64;
Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
Db 1 ATGGGATGGAGCTGGATCTTTCTCTTCCTCCTGTCAGGAACTGCAGGTGTCCACTCTGAG 60

Qy 61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120
Db 61 GTGCAGCTTGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120

Qy 121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACACTGGGTTAGACAGGCTCCT 180
Db 121 TGCAAGGCTTCTGGATACACCTTCACTGACTATAATATGCATTGGGTGAAGCAGGCCCAT 180

Qy 181 GGACAAGGGCTTGAGTGGATTGGATGGATTAATACTGAGACTGGTGAGCCAACATATGCA 240
Db 181 GGACAAGGACTTGAATGGATAGGATGGATTAATACTGAGACTGGTGAGCCAACATATGCA 240

Qy 241 CAGAAGTTCCAGGGCAAGGCCACAATTGCAGCAGACACATCCTCCAGCACAGCCTACATG 300
Db 241 CAGAAGTTCCAAGGCAAGGCCACATTGACTGTGGACAATTCCGGCGAGCACAGCCTACATG 300

Qy 301 GAACTTAGCTCCTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGGCCTGG 360
Db 301 GAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGGCAGAAGAGTTACTAT 360

Qy 361 TATATGGACTACTGGGGTCAAGGTACCCTGTCACCGTCTCCTCA 405
Db 361 GCTATGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCCTCA 405

RESULT 8
AAV61064
ID AAV61064 standard; cDNA to mRNA; 1768 BP.
XX
AC AAV61064;
XX
DT 18-JAN-1999 (first entry)
XX
DE Anti human Fas humanised antibody CH11 heavy chain HmuM cDNA.
XX
KW Humanised antibody; Fas; cell; monoclonal antibody; MAb; apoptosis;
KW autoimmune disease; rheumatoid arthritis; therapy; human;
KW antibody engineering; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/qualifiers
FT CDS 1..1767
FT /*tag= a
FT sig_peptide 1..57
FT /*tag= b
FT mat_peptide 58..1764
FT /*tag= c
XX
CN EP0901514-A.
XX
PD 24-SEP-1998.
XX
PF 20-MAR-1998; 98EP-0302113.
XX
PR 21-MAR-1997; 97JP-0067938.
XX
PA (SANY-) SANKYO CO LTD.
XX
PI Haruyama H, Nakahara K, Serizawa N, Takahashi F;
PI Yonehara S;
XX
DR WPI; 1998-481965/42.
DR P-PSDB; AAW71881.
XX
PT Production of anti Fas protein humanised antibodies - for use in
PT inducing apoptosis on Fas expressing cells in the treatment of
PT autoimmune diseases, especially rheumatoid arthritis
XX
PS Example 3; Page 108-110; 187pp; English.
XX
CC This cDNA sequence codes for a humanised anti Fas antibody CH11
CC heavy chain (see AAW71881), designated HmuM. HmuM is based on the
CC light chain (see AAW71888) of murine anti human Fas monoclonal
CC antibody CH11. The humanised sequence was designed following
CC selection of donor residues from CH11 to be grafted onto acceptor
CC molecule 21.28 9L. 2 light chain sequences (see AAW71886-87) have
CC been designed, and each can be used in combination with any of 4
CC light chain sequences (see AAW71876-79) to provide novel, claimed
CC humanised CH11 IgM antibodies that lack a J chain. These humanised
CC anti human Fas antibodies are capable of inducing apoptosis in cells
CC expressing Fas (e.g. synoviocytes) and are useful in the treatment
CC of autoimmune disease and chronic rheumatoid arthritis. DNA
CC sequences encoding the humanised antibodies are claimed, as are
CC vectors such as pHmuMI I including the HmuM nucleotide sequence,
CC and host cells such as Escherichia coli pHmuMI 1 (FERM BP-5864).
XX
SQ Sequence 1768 BP; 387 A; 564 C; 485 G; 332 T; 0 other;

Query Match 65.6%; Score 265.8; DB 19; Length 1768;
Best Local Similarity 78.5%; Pred. No. 4.4e-64;
Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
Db 1 ATGGGATGGAGCTGGATCTTTCTCTTCCTCCTGTCAGGAACTGCAGGTGTCCACTCTGAG 60

Qy 61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120
Db 61 GTGCAGCTTGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120

Qy 121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACACTGGGTTAGACAGGCTCCT 180
Db 121 TGCAAGGCTTCTGGATACACCTTCACTGACTATAATATGCATTGGGTGAAGCAGGCCCAT 180

Qy 181 GGACAAGGGCTTGAGTGGATTGGATGGATTAATACTGAGACTGGTGAGCCAACATATGCA 240
Db 181 GGACAAGGACTTGAATGGATAGGATGGATTAATACTGAGACTGGTGAGCCAACATATGCA 240

Qy 241 CAGAAGTTCCAGGGCAAGGCCACAATTGCAGCAGACACATCCTCCAGCACAGCCTACATG 300
Db 241 CAGAAGTTCCAAGGCAAGGCCACATTGACTGTGGACAATTCCGGCGAGCACAGCCTACATG 300

Qy 301 GAACTTAGCTCCTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGGCCTGG 360
Db 301 GAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGGCAGAAGAGTTACTAT 360

Qy 361 TATATGGACTACTGGGGTCAAGGTACCCTGTCACCGTCTCCTCA 405
Db 361 GCTATGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCCTCA 405

RESULT 9
AAA78272

```
ID   AAA78272 standard; DNA; 1768 BP.
XX
AC   AAA78272;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Anti human Fas immunoglobulin M heavy chain DNA sequence SEQ ID #87.
XX
KW   Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
KW   immunosuppression; autoimmune disease; treatment; rheumatism;
KW   anti Fas antibody; ss.
XX
OS   Synthetic.
XX
PN   JP2000154414-A.
XX
PD   06-JUN-2000.
XX
PF   17-SEP-1999;   99JP-0263984.
XX
PR   18-SEP-1998;   98JP-0264598.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2000-454476/40.
DR   P-PSDB; AAB12918.
XX
PT   Anti-human Fas humanizing antibody-containing antirheumatic agents
XX
PS   Example 2; Page 77-79; 109pp; Japanese.
XX
CC   The present invention relates to antirheumatic agents which comprise as
CC   active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC   does not include a J segment, has apoptosis inducing activity, and
CC   consists of a light and heavy chain polypeptide produced synthetically.
CC   The agents of the invention exhibit antirheumatic and immunosuppressive
CC   activity and can be used to treat autoimmune diseases, especially
CC   rheumatism. The IgM molecule used in the invention has human Fas-antigen
CC   binding properties. Included in the invention are nucleotide sequences
CC   of the IgM light and heavy chains (see AAA78267-A78272) and the
CC   corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
CC   nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
CC   AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also
CC   included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
CC   Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC   chains used in the invention are represented by sequences
CC   AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the
CC   invention are represented by sequences AAA78277-A78318 and
CC   AAA78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are
CC   represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer
CC   sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in
CC   the production of the agent of the invention.
XX
SQ   Sequence 1768 BP; 387 A; 564 C; 485 G; 332 T; 0 other;
```

Query Match 65.6%; Score 265.8; DB 21; Length 1768;
Best Local Similarity 78.5%; Pred. No. 3.4e-63;
Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

```
Qy          1 ATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
              ||||| |||| ||| ||| | |||| || |  |  |  | || |||| || ||||| ||
Db          1 ATGGGATGGAGCTGGATCTTTCTCTTCCTCCTGTCAGGAACTGCAGGCGTCCACTCTGAG 60

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
              || ||||| ||||||||||||||||||||||||||||||||||||  ||||||||||| |||
Db         61 GTGCAGCTTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120

Qy        121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACACTGGGTGAGACAGGCTCCT 180
              ||||| ||||| || ||||| |||||||| ||| ||| || ||||||| ||||| | |
Db        121 TGCAAGGCTTCTGGATACACCTTCACTGACTATAATATGCATTGGGTGAAGCAGGCCCAT 180

Qy        181 GGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
              ||| || ||||||| ||||| ||| |||| || |||| ||| | ||| |||||||
Db        181 GGAAAGAGCCTCGAATGGATGGGATATATTTATCCTTACAATGGTGGTACTGGCTACAAC 240

Qy        241 CAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACAGCACAGCCTATATG 300
              |||||||| ||| |||||||||||| |||||| |||| || ||||||||||||| |||
Db        241 CAGAAATTCAAGAGCAAGGCCACATTGACTGTTGACAATTCCGCCAGCACAGCCTACATG 300

Qy        301 GAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGCCTGG 360
              || || ||     |||||||||| || |||| || |||||||||||| |||     ||
Db        301 GAGCTGAGCAGCCTGAGATCTGAAGACACGGCTGTGTATTACTGTGCGAGAAGTTACTAT 360

Qy        361 TATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
              |||||||||||||||| || || |||| ||||||||||.||||
Db        361 GCTATGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 405
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RESULT 10
AAT42717
ID   AAT42717 standard; DNA; 424 BP.
XX
AC   AAT42717;
XX
DT   04-FEB-1997  (first entry)
XX
DE   HuMc3 VH coding sequence.
XX
KW   Humanised antibody; variable heavy region; buried residue modification;
KW   VH; HuMc3 VH; BA46 antigen; human; milk fat globule; HMFG; lactation;
KW   fat globule membrane; murine; mammal; epithelial cell; breast cancer;
KW   breast membrane glycoprotein; therapy; immunotherapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..418
FT                   /*tag= a
FT                   /product= HuMc3 VH (BR-M version)
FT
XX
PN   WO9608565-A2.
XX
PD   21-MAR-1996.
XX
PF   14-SEP-1995;   95WO-US11683.
XX
PR   07-JUN-1995;   95US-0487598.
PR   16-SEP-1994;   94US-0307868.
XX
PA   (CANC-) CANCER RES FUND CONTRA COSTA.
XX
PI   Ceriani RL, Do Couto FJR, Peterson JA;
XX
DR   WPI; 1996-179941/18.
DR   P-PSDB; AAW06442.
XX
PT   Recombinant Mc3 antibody which binds BA46 antigen of HMFG -
PT   comprises a modified heavy or light chain variable region, useful in
PT   the diagnosis and therapy of breast cancer
XX
PS   Claim 14; Fig 18; 91pp; English.
XX
CC   This sequence represents the coding sequence for the variable heavy (VH)
CC   chain of the humanised murine antibody HuMc3 VH.  The Mc3 VH sequence was
CC   humanised using the buried residue modification technique, where
CC   important non human framework residues are unaffected.  The Mc3 antibody
CC   binds to the BA46 antigen of the human milk fat globule (HMFG).  The milk
CC   fat globule membrane is derived from the apical surface of the mammalian
CC   epithelial cell during lactation, and therefore is a source for breast
CC   membrane glycoproteins.  The antibody can be used in an in vitro method
CC   to detect a HMFG antigen (or antigen fragment), and to diagnose the
CC   presence of the antigen in a subject.  The antibody can also be used to
CC   deliver an agent to a target (within a subjects body), containing a HMFG
CC   antigen.  The antibodies can also be used for diagnosis, prognosis, and
CC   therapeutic applications of breast cancer.  As the humanised antibodies
CC   retain their high affinity binding to the antigen, they are useful for
```

```
CC   immunodiagnostic and immunotherapeutic applications in humans.
XX
SQ   Sequence 424 BP; 106 A; 102 C; 112 G; 104 T; 0 other;

  Query Match             62.8%;  Score 254.4;  DB 17;  Length 424;
  Best Local Similarity   78.2%;  Pred. No. 5.1e-60;
  Matches  314;  Conservative    0;  Mismatches   95;  Indels    3;  Gaps    1;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTCCTGGTTACTACAGCTACAGGTGTCCACTCCCAG 60
              ||| |||| |||| |||| || | | | | ||||||| ||||| ||
Db         11 ATGAAATGCACCTGGCTCATCTTCCTCCTGGTCGCAGCAGCTACAGGTGTCCACTCTGAG 70

Qy         61 GTCCAGCTGCAACAGTCTGGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATCTCC 120
              ||||||||||||||||||| |||||||||||||||||    |||||||||| |||
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Qy        181 GGAAGGGGTTAGTGGATGGATAGGACTAATAATATTAACTATGCAGAATATGCTGAAGTC 240
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Db        191 GGAATGAACTTGAGTGGATGGGATGGATAAACACCAACACTGGAGAGCCAACATATGCT 250

Qy        241 CAGGGACGGTTCACCTTCTCTTTGGAAACCTCTGCCAGCACTGCCTATTTGCAGATCAAC 300
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Db        251 CAGGGACGGTTCGCGGGCAAGGGCGCAATTAACTGTAGCAACAGTCAAGGAACTGCCTAC 310

Qy        301 GGAACTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGGCTGG 360
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Db        311 GACCTCAGCAGTCTGAGATCTGAGGACACGGCACTCTATTTCTGTGCAAGAGCGTTGGAGA 370

Qy        361 TA   TATAGACTACTGGGGTCAAGGAACCCTGGTCACCGTCTCCTCA 405
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Db        371 TATACTATGGAACATTTGGCAGTGGAACCCAAGTCATCGTCTCCTCA 415


RESULT 11
AAQ66700
ID   AAQ66700 standard; cDNA; 451 BP.
XX
AC   AAQ66700;
XX
DT   16-NOV-2000  (first entry)
XX
DE   DREG 200 Humanized antibody heavy chain variable region.
XX
KW   DREG 200; L-selectin; IFNAM 1; Mel 14; LAM 1;
KW   humanized antibody; immunoglobulin; Ig; IgG1; IgG4;
KW   complementarity-determining region; CDR; monoclonal antibody; MAb;
KW   framework; light chain; heavy chain; transgenic animal.
KW   monoclonal antibody; receptor antibody; Ea; transgenic animal; ss.
XX
OS   Mus sp.; Homo sapiens.
XX
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FT   sig_peptide     1..57
FT                   /*tag= b
FT   mat_peptide     58..451
FT                   /*tag= c
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PN   WO0112232-A.
XX
PD   22-FEB-2001.
XX
PF   16-NOV-2000;    2000WO-US031412.
XX
PR   17-AUG-1999;    99DE-1039040.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT.
XX
PI   Co MS;
XX
DR   WPI; 1994-199974/24.
DR   P-PSDB; AAR55556.
XX
PT   New humanised antibody specific for L-selectin - with murine CDRs
PT   and human framework regions, inhibits binding of neutrophils to
PT   endothelial cells and useful for treating or preventing
PT   inflammation.
XX
PS   Disclosure; Fig. 4B; 60pp; English.
XX
CC   An L-selectin specific IgG1 or IgG4 humanized antibody has CDRs
CC   corresponding to those of mouse MAb DREG 200 and heavy and light
CC   chain variable region frameworks of the human acceptor antibody Eu.
CC   Nucleotide and aa sequences are provided for the DREG-200 light
CC   (AAQ66699, AAR55554) and heavy (AAQ66700, AAR55556) chain variable
CC   regions and the humanized DREG 200 light (AAQ66701, AAR55555) and heavy
CC   (AAQ66702, AAR55556) chain variable regions. The humanized antibodies
CC   can be produced economically in large quantities by expression in
CC   mammalian cell culture or in transgenic animals.
XX
SQ   Sequence 451 BP; 120 A; 105 C; 116 G; 110 T; 0 other;

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Qy        121 TGCAAAACTTCCGGCTACACATTCACTGATTATGCTATACACTGGGTGAAGCAGAGCCAT 180
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Db        132 TGCAAGGCTTCTGGATACACCTTCACTAACTATGGAATGAACTGGGTGAAGCAGGCTCCA 191

Qy        181 GGAAAGAGCTTAGAGTGGATTGGATGGATAAACACCTACACTGGAGAACCAACATATGCT 240
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Qy        241 CAGGAAGTTAAAGGGCGGATTGACTTTTCTTTGGAAACCTCTGCAAGCACTGCCTACTTG 300
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Qy        301 CAGATCAACAACCTCAAAAATGAGGACACGGCTACATATTTCTGTGCAAGAGGGGGGTTA 360
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Db        312 CAGATCAGCAACCTCAAGAATGAGGACATGGCTACGTATTTCTGTGCAAGATCGATTACT 371

Qy        361 ACGACGGTAGGTTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA 415
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Db        372 ACGACGGTGGGTTTTACTTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA 426


RESULT 12
AAV70080
ID   AAV70080 standard; DNA; 2971 BP.
XX
AC   AAV70080;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Anti Fas humanised antibody BFE7A heavy chain DNA.
XX
KW   BFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW   apoptosis; BFE7A; autoimmune disease; Hashimoto's disease;
KW   systemic lupus erythematosus; graft versus host disease;
KW   Sjogren syndrome; pernicious anaemia; Addison's disease;
KW   scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW   rheumatoid arthritis; autoimmune haemolytic anaemia;
```

```
KW   myasthenia gravis; multiple sclerosis; Basedow's disease;
KW   thrombopenia purpura; insulin-dependent diabetes; allergy;
KW   atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW   glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW   transplant rejection; therapy; ds.
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OS   Homo sapiens.
OS   Synthetic.
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PD   08-OCT-1998.
XX
PF   30-MAR-1998;    98AU-0059701.
XX
PR   08-OCT-1997;    97JP-0276064.
PR   01-AUG-1997;    97JP-0082953.
PR   25-JUN-1997;    97JP-0169088.
XX
PA   (SANY ) SANKYO CO LTD.
XX
PI   Akio S;  Hideyuki H;  Hiroko Y;  Jun O;  Kimihisa I;
PI   Masahiko O;  Nobutusa S;  Shin Y;  Tohru T;
XX
DR   WPI; 1998-541440/47.
DR   P-PSDB; AAW83037.
XX
PT   New antibodies and proteins bind conserved epitope of Fas antigen -
PT   used to evaluate drugs in animal models and to treat Fas-associated
PT   diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT   myocarditis, hepatitis and AIDS
XX
PS   Claim 27; Page 223-225; 292pp; English.
XX
CC   This nucleotide sequence codes for the HV type humanised heavy
CC   chain (see AAW83037) of murine anti-human Fas monoclonal antibody
CC   HFE7A. It was prepared from plasmid pqHSL7A62 (see AAV70079) by
CC   PCR amplification (see AAV70115-17), and includes humanising R44G
CC   and A76T amino acid substitutions. Host cell Escherichia coli
CC   pqHPDHV3 SANK 70298 harbors plasmid pqHPDHV3 carrying a fusion
CC   fragment of the humanised HV type HFE7A heavy chain and DNA
CC   encoding human IgG1 constant region, and is deposited as
CC   FERM BP-5273 (claimed). The invention provides methods for
CC   producing humanised antibodies by culturing host cells. Humanised
CC   versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
CC   of inducing apoptosis in abnormal cells expressing Fas, and of
CC   inhibiting Fas-induced apoptosis in normal cells. The humanised
CC   antibodies are used to evaluate, in animal models, treatments of
CC   diseases that involve Fas/Fas ligand interactions, and also to
CC   treat such diseases, including autoimmune disease (e.g. systemic
CC   lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC   Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC   Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC   autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC   multiple sclerosis, Basedow's disease, thrombopenia purpura and
CC   insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC   myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC   anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ   Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;

  Query Match          62.6%;  Score 258.6;  DB 19;  Length 2071;
  Best Local Similarity  77.6%;  Pred. No. 7.8e-60;
  Matches  326;  Conservative    0;  Mismatches   79;  Indels   15;  Gaps    1;

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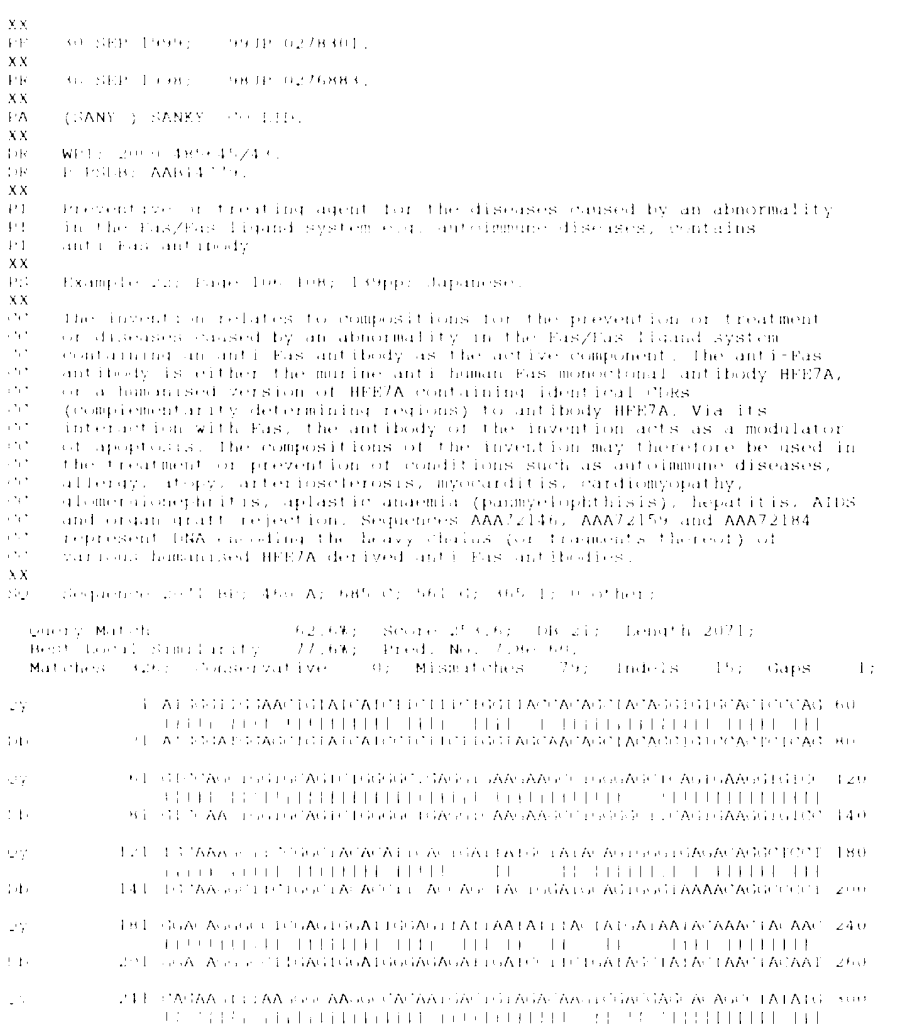
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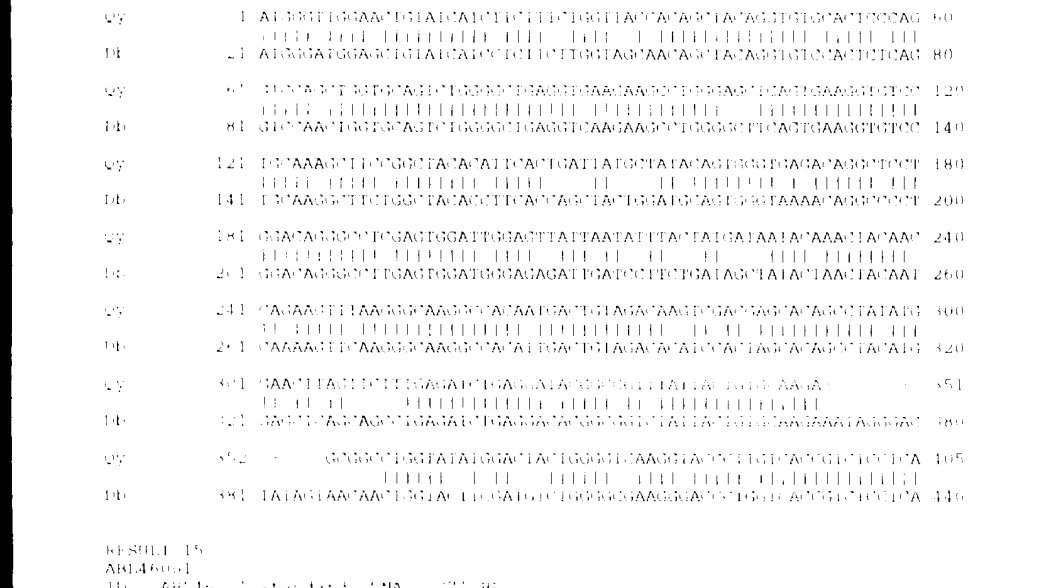
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AC   AAA72184;
XX
DT   24-NOV-2000 (first entry)
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DE   DNA encoding humanised anti-Fas antibody heavy chain, SEQ ID NO:116.
XX
KW   Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5820;
KW   murine; humanised antibody; complementarity determining region; CDR;
KW   human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW   autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW   cardiomyopathy; glomerulonephritis; aplastic anaemia; poliomyelopathisis;
KW   hepatitis; AIDS; graft rejection; heavy chain; ds.
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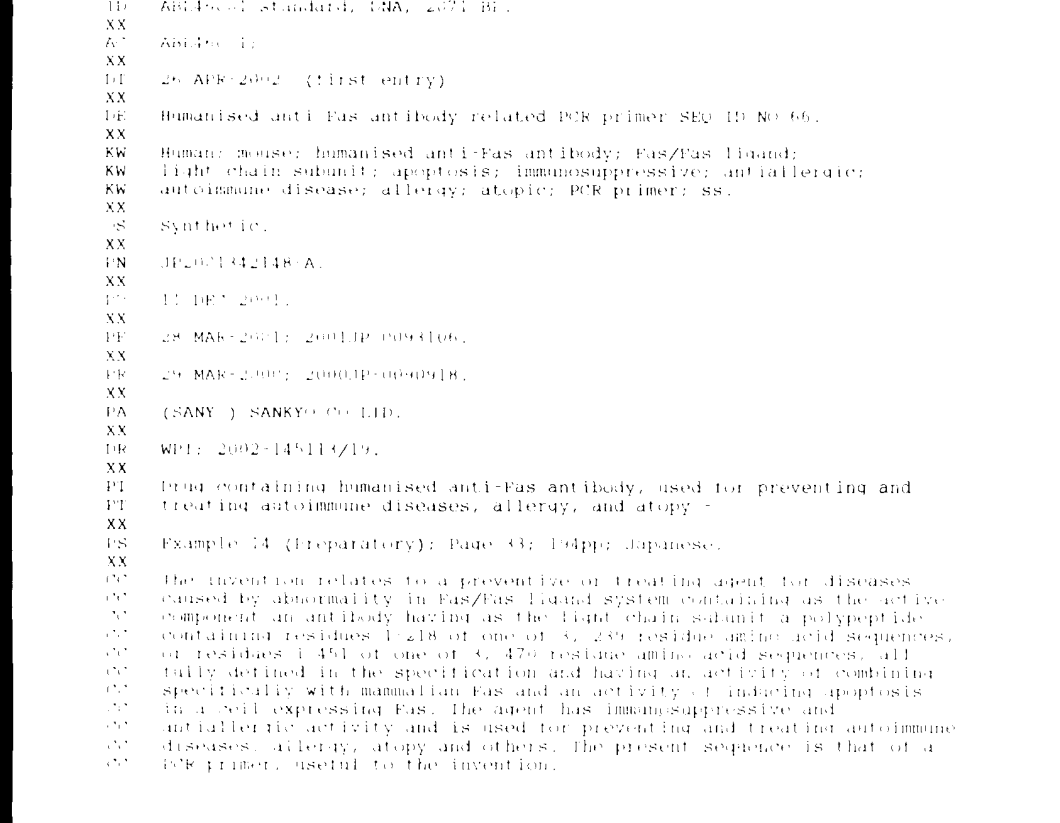
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XX
PA   (SANY ) SANKYO CO LTD.
XX
PI   Furukawa N, Hatayama H, Nakahara K, Takaki I, Takahashi T;
XX
DR   WPI; 2000-258950/23.
DR   P-PSDB; AAW90929.
XX
PT   Novel humanized anti Fas antibody, useful for treating or preventing e.g.
PT   inflammatory or autoimmune disease, induces apoptosis selectively in
PT   cells with abnormal Fas Fas ligand systems
XX
PS   Example reference 22; Page 148-150; 263pp; English.
XX
CC   This invention describes a novel humanized anti Fas antibody-like
CC   molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC   ligand system, by binding to Fas on the cell surface, and prevents
CC   apoptosis in cells with a normal system, by inhibiting binding between
CC   Fas and its ligand. The products of the invention have anti inflammatory,
CC   anti-anemic, antidiabetic, anti-allergic, anti arthritic, antiviral,
CC   immunomodulatory, dermatological, immunosuppressive, thymomimetic,
CC   antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC   antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC   apoptosis by binding to cell surface Fas or inhibit it by competitive
CC   inhibition of ligand binding. (I) are used to treat and/or prevent
CC   diseases associated with the Fas/Fas ligand system, especially systemic
CC   lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC   versus host disease, Sjogren's syndrome, pernicious or hypoplastic
CC   anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC   disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC   multiple sclerosis, Basedow's disease, thrombopenia purpura, allergy,
CC   dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC   cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC   (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC   inhibit apoptosis in normal cells but selectively induce it in abnormal
CC   cells. They bind to both human and murine Fas, so can be evaluated in
CC   murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC   the native ligand, do not induce liver disease, and have reduced risk of
CC   inducing a human anti-murine antibody response. This sequence encodes
CC   a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
CC   the method described in the invention.
XX
SQ   Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;

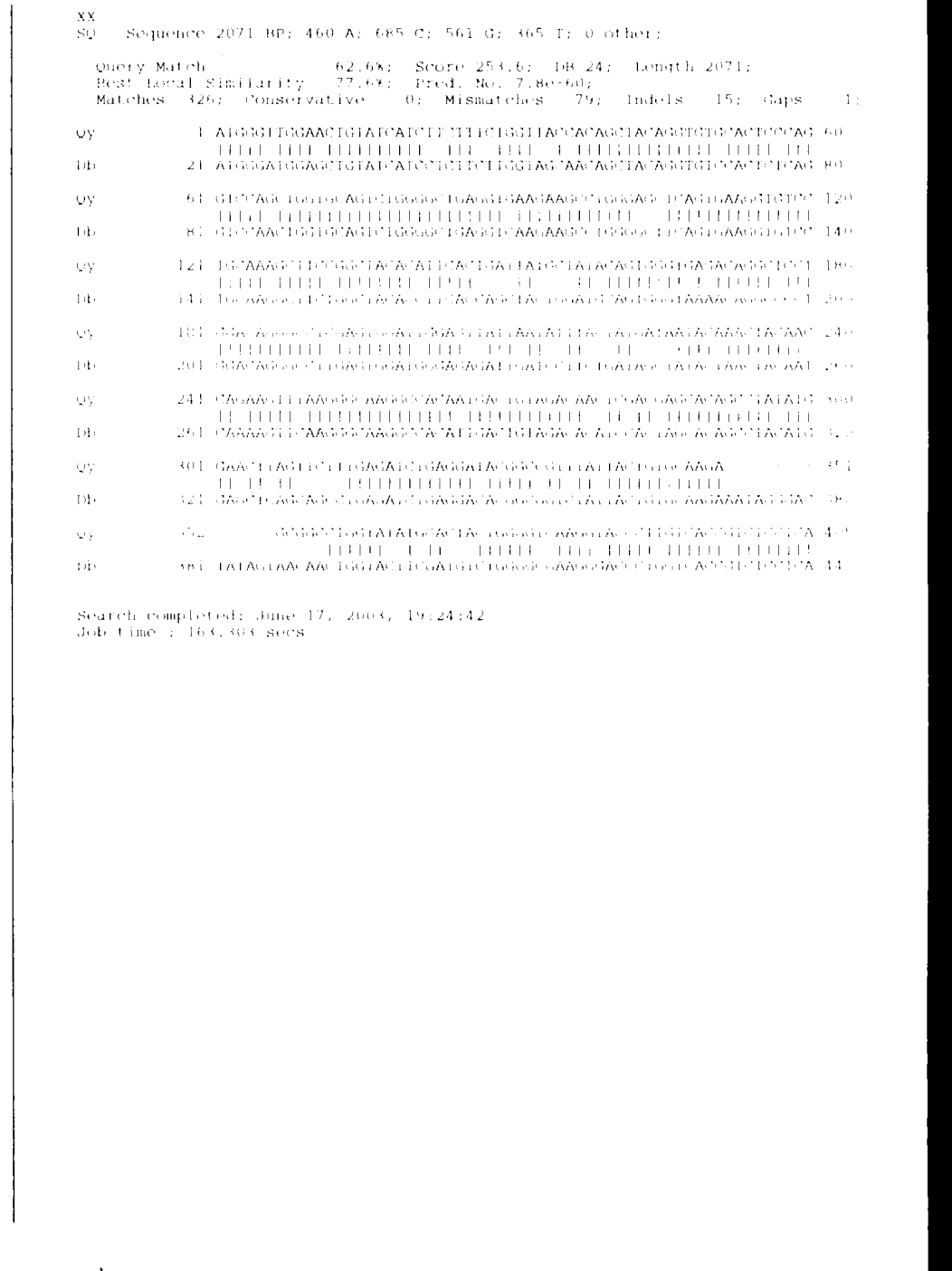
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RESULT 14
AAA11622
ID   AAA11622 standard; DNA; 2071 BP.
XX
AC   AAA11622;
XX
DT   08-AUG-2000 (first entry)
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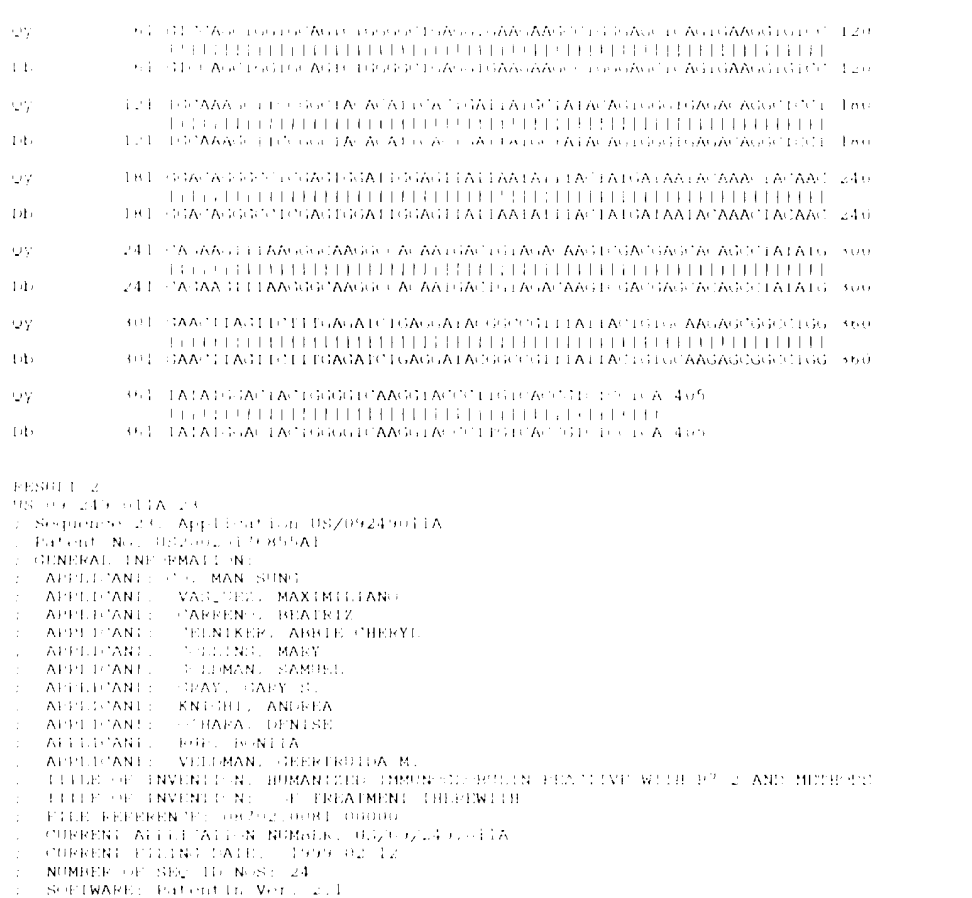
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13	248.8	61.4	2077	9	US-10-216-484-88	Sequence 88, Appl
14	245.6	60.6	2077	9	US-10-216-484-156	Sequence 156, App
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16	244.8	60.4	409	9	US-10-160-232-42	Sequence 42, Appl
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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: [illegible]
; APPLICANT: VAITAITIS, MARYBETH ANN
; APPLICANT: [illegible]
; APPLICANT: [illegible]
; APPLICANT: [illegible]
; APPLICANT: [illegible]
; APPLICANT: [illegible]
; APPLICANT: OKADA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELLMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 887021.3381 US00A
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized
; OTHER INFORMATION: murine anti-human B7-2 heavy chain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(405)
US-09-249-011A-5

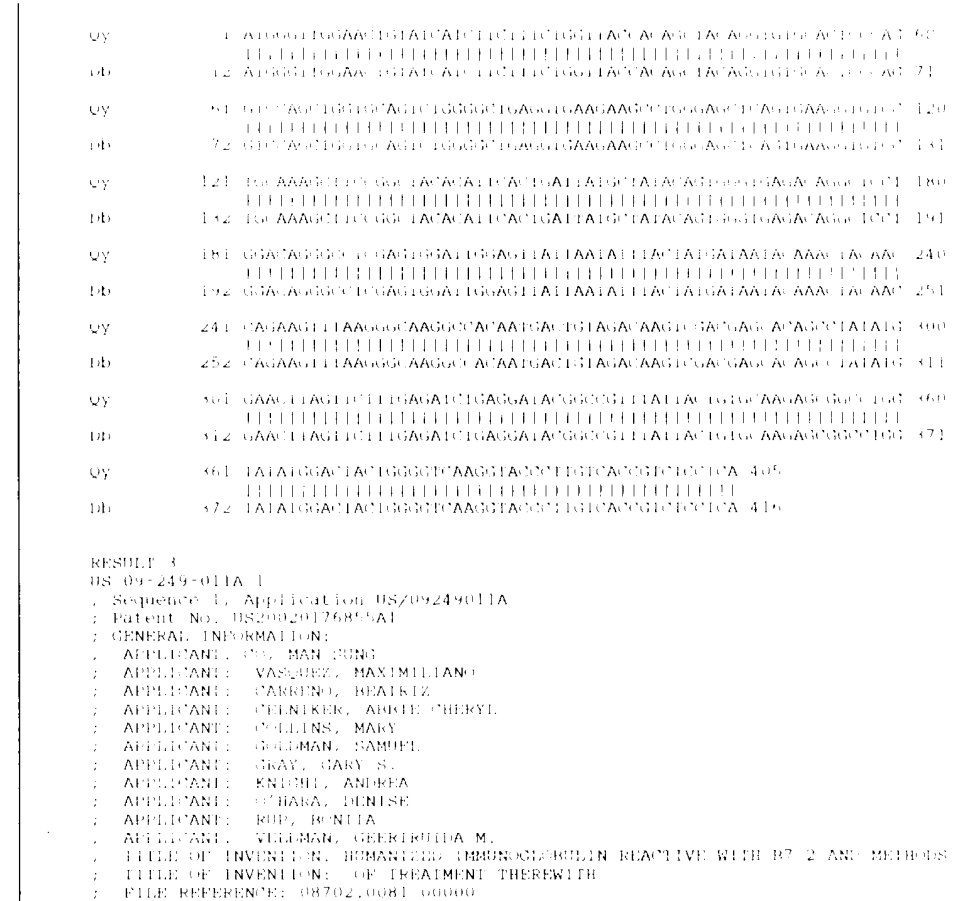
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Best Local Similarity 100.0%; Pred. No. 2.3e-123;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 [illegible] 60
Db 1 [illegible] 60



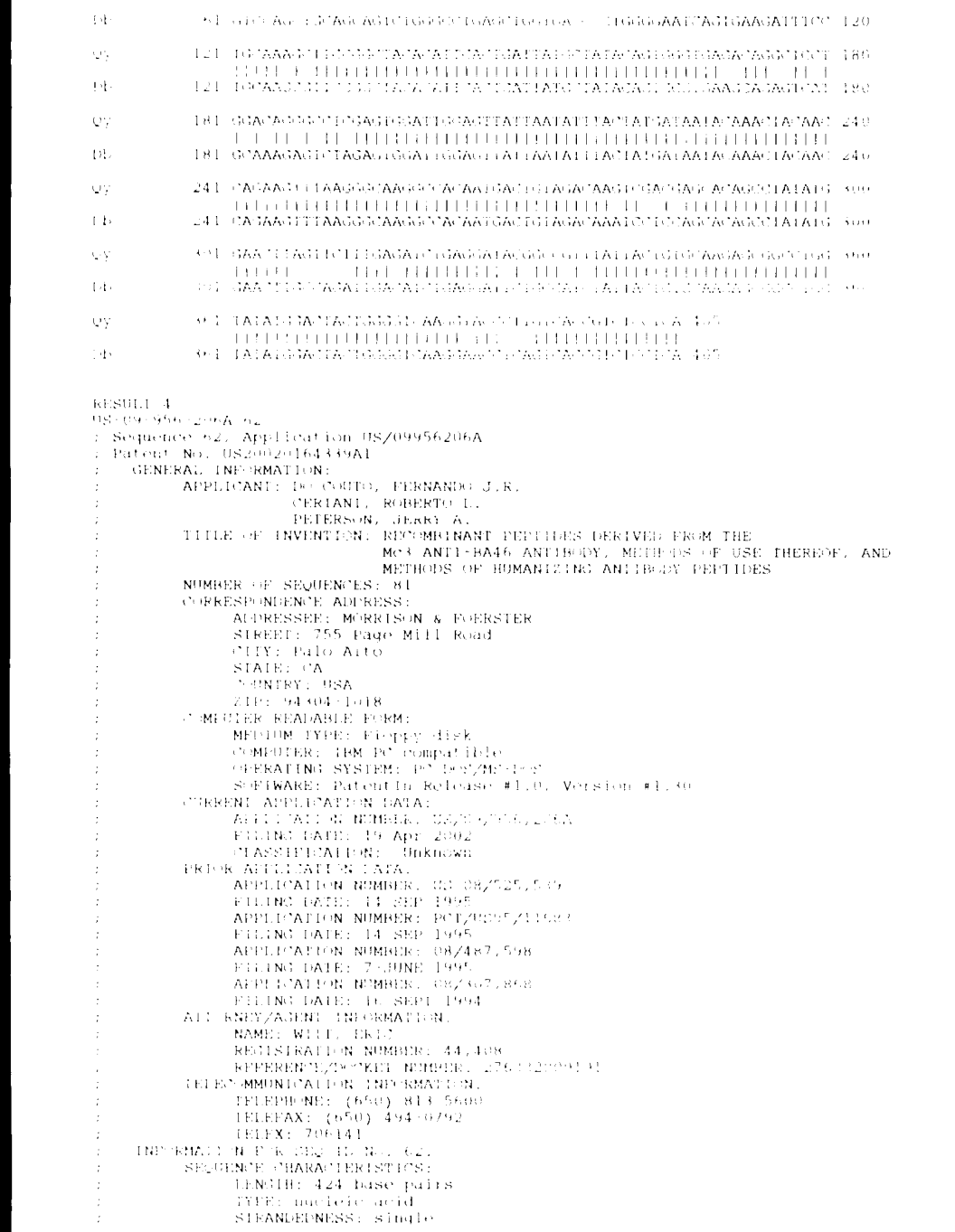
RESULT 2
US-09-249-011A-24
; Sequence 24, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: KIM, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: PELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: KHAKA, DENISE
; APPLICANT: RUP, RONTIA
; APPLICANT: VELLOMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7.2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)..(417)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (553)..(648)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1311)..(1376)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1470)..(2121)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1553)..(1599)
US-09-249-011A-24

Query Match 100.0%; Score 405; DB 9; Length 2249;
Best Local Similarity 100.0%; Pred. No. 4.7e-122;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



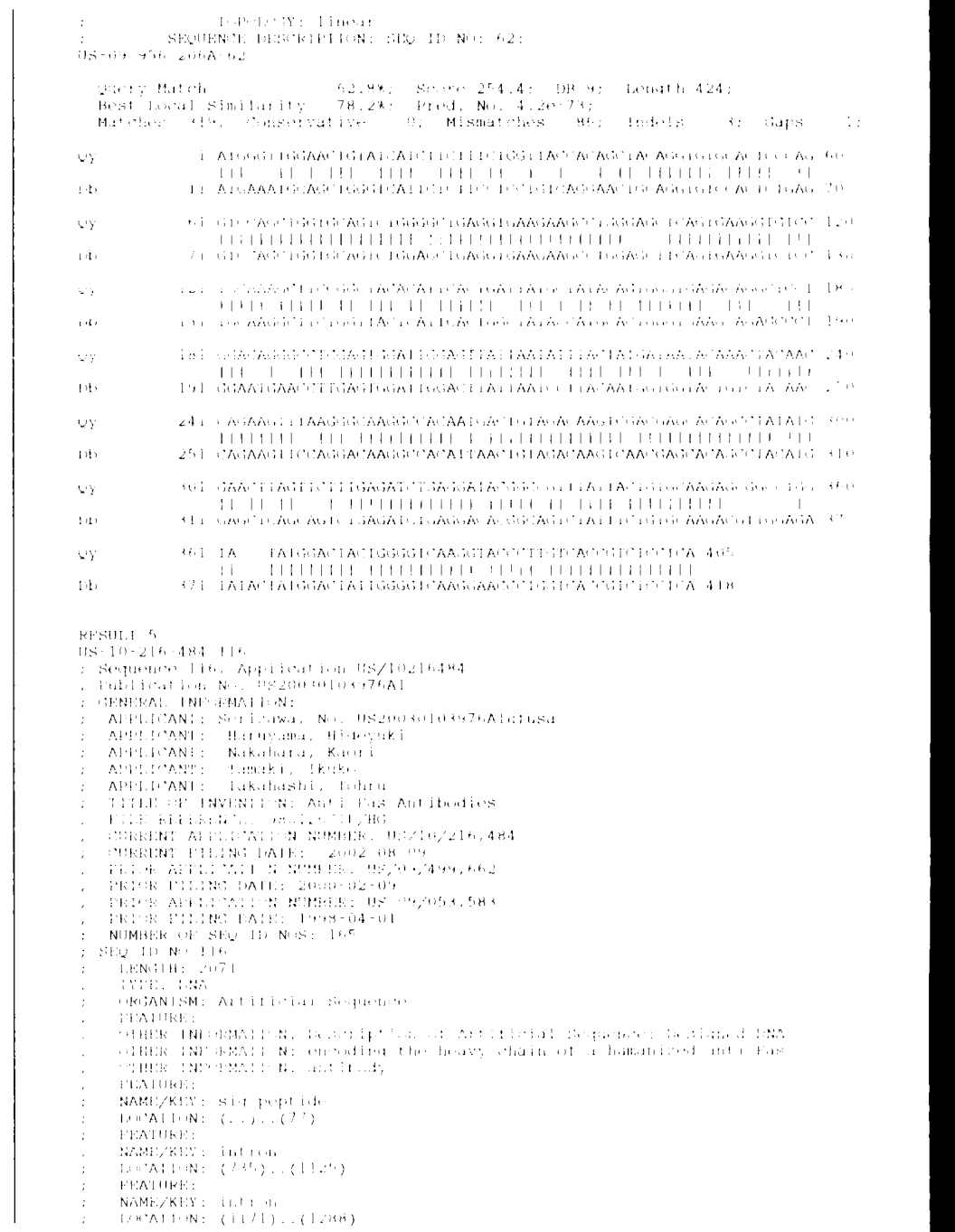
RESULT 3
US-09-249-011A-1
; Sequence 1, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: KIM, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: PELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: KHAKA, DENISE
; APPLICANT: RUP, RONTIA
; APPLICANT: VELLOMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7.2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Murine sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(405)
; OTHER INFORMATION: Anti-B7.2 heavy chain
US-09-249-011A-1

Query Match 82.6%; Score 334.6; DB 9; Length 405;
Best Local Similarity 89.1%; Pred. No. 2.3e-99;
Matches 361; Conservative 9; Mismatches 44; Indels 0; Gaps 0;

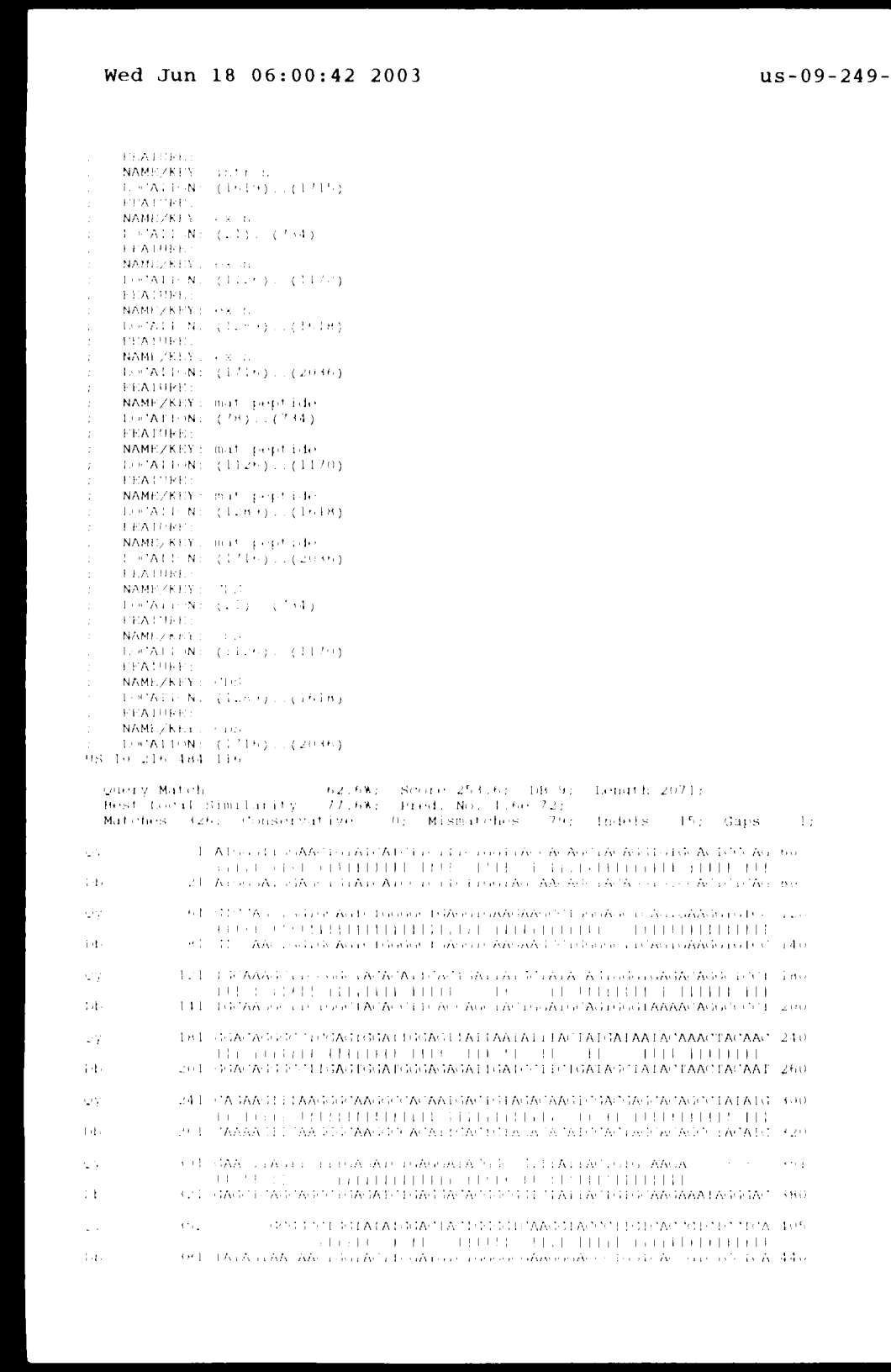


RESULT 4
US/09/956,206A/52
; Sequence 52, Application US/09956206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: De Cotto, Fernando J.R.
; Cerlani, Roberto L.
; Peterson, Jeaky A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; Mc3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,549
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/US95/11523
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,598
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/307,868
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEIL, ERIC
; REGISTRATION NUMBER: 44,438
; REFERENCE/DOCKET NUMBER: 27622/29941
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-956-206A-52

Query Match 62.9%; Score 254.4; DB 9; Length 424;
Best Local Similarity 78.2%; Pred. No. 4.2e-73;
Matches 435; Conservative 0; Mismatches 96; Indels 8; Gaps 1;



RESULT 5
US/10-216-484-116
; Sequence 116, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Seriwaw, No. US2003010397GA1Gitusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 0648.2031/BG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/054,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 116
; LENGTH: 2071
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Isolated DNA
; OTHER INFORMATION: encoding the heavy chain of a humanized anti-Fas
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (...)...(77)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (735)..(1125)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1171)..(1288)



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;   LENGTH: 4210
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-897-006-5

  Query Match             62.5%;  Score 254;  DB 10;  Length 4210;
  Best Local Similarity   76.5%;  Pred. No. 3.5e-72;
  Matches  317;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTGGAACTGTATCATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
              ||||| ||| |||||||||| |||| |||| | ||||||||||||||| |||||||||
Db        852 ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCCCAG 911

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGCACCTCAGTGAAGGTGTCC 120
              |||||||||||| || || |||||||| || ||||| ||||||   |||||||||||| |||
Db        912 GTCCAGCTGTCTCCAATCAGGGGCTGAAGTCAAGAAACCTGGGTCATCAGTGAAGGTCTCC 971

Qy        121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGCTCCT 180
              ||||| ||||| |||||||| || |||   ||     | || ||||| || ||||| |||
Db        972 TGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGCTGCACTGGGTTCAGCAGGCACCT 1031

Qy        181 GGACAAGGGCTTGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
              |||||||| || || ||||||||   |||||| |   ||||| ||||   | |||||
Db       1032 GGACAGGGTCTGGAATGGATTGGAATCATTAATCCTAGGAATGATTATACTGACTACAAT 1091

Qy        241 CAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGAGCAGCACAGCCTATATG 300
              ||||| || |||| |||||||||||| |||| |||| | || || |  |||||||| |||
Db       1092 CAGAACTTCAAGGACAAGGCCACAATAACTGCAGACAAATCCACCAATACAGCCTACATG 1151

Qy        301 GAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGGCCTGG 360
              || || ||    |||| |||||||| ||||| |||||| |||||||||  ||
Db       1152 GAGCTGAGCAGCCTGAGGTCTGAGGACACGGCATTTTATTTTTGTGCAAGAAGGGATATT 1211

Qy        361 TATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
                 || |  |||||||| |||| ||| |||||||||||||||
Db       1212 ACTACGTTCTACTGGGGCCAAGGCACCACGGTCACCGTCTCCTCA 1256


RESULT 8
US-10-216-484-142
; Sequence 142, Application US/10216484
; Publication No. US20040103976A1
; GENERAL INFORMATION:
;  APPLICANT: Setizawa, No. US20040103976Alutusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Hideo
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 980126CIP/BC
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/249,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 142
;   LENGTH: 2073
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
;   OTHER INFORMATION: encoding the heavy chain of a humanized anti Fas
;   OTHER INFORMATION: antibody
;   FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: (23)..(79)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (747)..(1127)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1173)..(1290)
;   FEATURE:
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;   LOCATION: (1621)..(1717)
;   FEATURE:
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;   NAME/KEY: exon
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;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1291)..(1620)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1718)..(2038)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (80)..(736)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (1128)..(1172)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (1291)..(1620)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (1718)..(2038)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (23)..(736)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1128)..(1172)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1291)..(1620)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1718)..(2038)
US-10-216-484-142

  Query Match             62.2%;  Score 252;  DB 9;  Length 2073;
  Best Local Similarity   77.4%;  Pred. No. 5.4e-72;
  Matches  325;  Conservative    0;  Mismatches   80;  Indels   15;  Gaps    1;

Qy          1 ATGGGTTGGAACTGTATCATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
              ||||| ||| |||||||||| |||| |||| | |||||||||||||| || || |||
Db         23 ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCATTCTCAG 82

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGCAGCTCAGTGAAGGTGTCC 120
              ||||| |||||||| |||||||||||||| ||||||||||   ||||||||||||| |||
Db         83 GTCCAACTGAAGCAGTCTGGACCTGAGCTGAAGAAGCCTGGGGCTTCAGTGAAGGTGTCC 142

Qy        121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGCTCCT 180
              ||||| ||||| |||||||| ||||   ||     || || |||||| | |||||| |||
Db        143 TGCAAGGCTTCTGGCTACACCTTCACTAGCTACTGGATGCAGTGGGTAAAACAGAGGCCT 202

Qy        181 GGACAAGGGCTTGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
              |||||||| || |||||||| |||| ||| || ||   || |  |||||||| |||||
Db        203 GGACAGGGACTTGAGTGGATTGGGAGAATTGATCCTTCTGATAGCTATACTAACTACAAT 262

Qy        241 CAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGAGCAGCACAGCCTATATG 300
              || ||||| |||||||||||||| ||||||||||||   || || ||||||||||| |||
Db        263 CAAAAATTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 322

Qy        301 GAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA          351
              || || ||    |||||||||||| |||| || ||||||||||||||
Db        323 GAGCTCAGCAGCCTGAGATCTGAGGACACGGCGGTCTATTACTGTGCAAGAAAATAGCTAC 382

Qy        352 ---GCGGGCCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
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[illegible]

RESULT 9
US-10-216-484-144
; Sequence 144, Application US/10216484
; Publication No. US20030104976A1
; GENERAL INFORMATION:
; APPLICANT: Seriwa, No. US20030104976Alutosa
; APPLICANT: Hanayama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Imaoki, Ikuko
; APPLICANT: Takahashi, Ichiro
; TITLE OF INVENTION: Anti Fas Antibodies
; FILE REFERENCE: 980126CIP/BG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/276,583
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 144
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene coding
; OTHER INFORMATION: encoding the heavy chain of a humanized anti Fas
; OTHER INFORMATION: antibody
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (23)..(77)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (78)..(1127)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1178)..(1200)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1621)..(1717)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (23)..(736)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1128)..(1172)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1201)..(1536)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1718)..(2038)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (89)..(736)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1128)..(1172)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1201)..(1529)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1718)..(2038)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23)..(736)
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; NAME/KEY: CDS
; LOCATION: (1128)..(1172)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1201)..(1529)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1718)..(2038)
US-10-216-484-144

Query Match 62.2%; Score 252; DB 9; Length 2073;
Best Local Similarity 77.4%; Pred. No. 5.4e-72;
Matches 325; Conservative 0; Mismatches 80; Indels 15; Gaps 1;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTACTACAGCTACAGGTGTGCACTCCCAG 60
||||| |||| |||||||||| |||| |||| | |||||||||||||| || || |||
Db 23 ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCATTCTCAG 82

Qy 61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGTGTCC 120
||||| |||||||||||||||||||||| |||||||||||| ||.|||||||||||
Db 83 GTCCAACTGCTGCAGCAGTCAGGGCTGAGGTCAAGAAGCCTGGGGCCTCAGTGAAGATGTCC 142

Qy 121 TGCAAAGCTTCTGGCTACACATTCACTGATTATGCTATACACTGGGTGAAGCAGAGCCCTGCT 180
||.|| ||||| |||||||| |||| || || |||||||| | ||||| |||
Db 143 TGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTAAAACAGAGGCCTGCT 202

Qy 181 CGACAAGGCCTCGAGTGGATTGGAGCTATTAATATTTACTATGATAATACAAACTACAAT 240
|||||||| || |||||||| |||| ||| || || || |||| |||||||
Db 203 CGACAAGGACTTGAGTGGATCGGAGCTATTAATCCTGGTAGTGGTAATACTAACTACAAT 262

Qy 241 GAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACACATCCTCCAGCACAGCCTACATG 300
|| |||| |||||||||||||||||||| |||||||||| || || |||||||||||
Db 263 GAGAAGTTCAAGGGCAAGGCCACAATAACTGCAGACAAATCCTCCAGCACAGCCTACATG 322

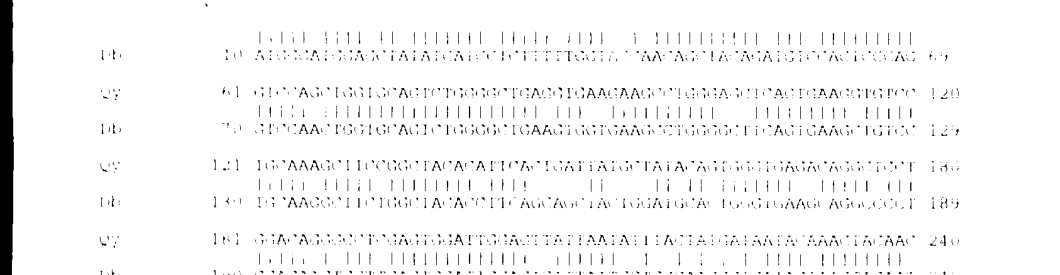
Qy 301 GAACTCAGCAGCCTGACATCTGAGGACACTGCAGTCTATTACTGTGCAAGAGA 351
|| || || |||||||||||| |||| || |||||||||||||||| |||||
Db 323 GAGCTCAGCAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCAAGAAATAGGGAC 382

Qy 352 -GGGGCTGGTATAGGACTACTGGGGTCAAGGTACCCTGGTCACCGTCTCCTCA 405
|||||| | || |||||| ||||||| || |||||||||||||||||
Db 383 TATAGTAACGACTGGTACTTCGATGTCTGGGGCCAAGGTACACTGGTCACCGTCTCCTCA 442

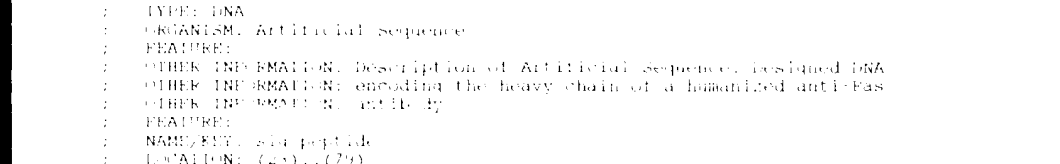
RESULT 10
US-10-233-996-43
; Sequence 43, Application US/10233996
; Publication No. US20030099676A1
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang Yull
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES LB 0050 AND LB 0050 SPECIFIC FOR HUMAN
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING SAID HUMANIZED ANTIBOD
; FILE REFERENCE: 4363.0102P
; CURRENT APPLICATION NUMBER: US/10/233,996
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene coding
; OTHER INFORMATION: for variable region of heavy chain of humanized
; OTHER INFORMATION: antibody B-4B4 1
US-10-233-996-43

Query Match 62.1%; Score 251.6; DB 9; Length 423;
Best Local Similarity 77.5%; Pred. No. 8.5e-72;
Matches 423; Conservative 0; Mismatches 84; Indels 9; Gaps 1;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTACTACAGCTACAGGTGTGCACTCCCAG 60



RESULT 11
US-10-216-484-146
; Sequence 146, Application US/10216484
; Publication No. US20030040976A1
; GENERAL INFORMATION:
; APPLICANT: Seriawa, No. US20030040976A1ttnsa
; APPLICANT: Hirayama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Iwaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti Fas Antibodies
; FILE REFERENCE: 980126^IP/HC
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/4xx,5x2
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,5xx
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 1x5
; SEQ ID NO 146
; LENGTH: 2x78
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
; OTHER INFORMATION: encoding the heavy chain of a humanized anti-Fas
; OTHER INFORMATION: mAb Hy
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (23)..(79)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (737)..(1127)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (1174)..(1290)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (1621)..(1717)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (23)..(736)
; FEATURE:
; NAME/KEY: exon
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; LOCATION: (80)..(736)
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; FEATURE:
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; LOCATION: (1718)..(2038)
; FEATURE:
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; LOCATION: (23)..(736)
; FEATURE:
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; LOCATION: (1291)..(1620)
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; NAME/KEY: CDS
; LOCATION: (1718)..(2038)
US-10-216-484-146



RESULT 12
US-10-216-484-74
; Sequence 74, Application US/10216484
; Publication No. US20030040976A1
; GENERAL INFORMATION:
; APPLICANT: Seriawa, No. US20030040976A1ttnsa
; APPLICANT: Hirayama, Hideyuki
; APPLICANT: Nakahara, Kaori

; APPLICANT: Imaki, Hideki
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti Fas Antibodies
; FILE REFERENCE: 9801/PCT/EP/BG
; CURRENT APPLICATION NUMBER: US/09/499,662
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 09/054,599
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 74
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA encoding
; OTHER INFORMATION: the partial peptide of the heavy chain of a
; OTHER INFORMATION: humanized anti Fas antibody
; FEATURE:
; NAME/KEY: misc
; LOCATION: (21)..(455)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (78)..(455)
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (21)..(77)
US 09-249-011B-5

Query Match 61.4%; Score 248.8; DB 9; Length 457;
Best Local Similarity 76.9%; Pred. No. 4e-71;
Matches 423; Conservative 0; Mismatches 82; Indels 15; Gaps 1;

Qy 1 ATGGGGTCGAACTGTATCATCTTCTTCCTGGTTGCTGTTGCTACAGGTGTGCACTCCCAG 60
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Db 21 ATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCTCAG 80

Qy 61 GTCCAGCTTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGAGTCAGTGAAGGTGTCC 120
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Db 81 GTCAAAAAGCCTGGGGCCTCAGTGAAGATATCCTGCAAGGCTTCAGGCTACACCTTCACC 140

Qy 121 TGCAAAGCTTCTGGATACACATTCACTAGCTATGATATAAACTGGGTGAAGCAGAGGCCTGGA 180
|| ||| ||| |||||||| |||| || || |||||||| | |||||| |||
Db 141 TGCAAGGCTTCTGGCTACACCTTCACCAGCTATGATATCAACTGGATAAAGCAGAGGCCTGGA 200

Qy 181 CAAGGGCTTGAGTGGATTGGATGGATTTATCCTAGAGATGGTAGTACTAAGTACAATGAGAAG 240
|||||| | || |||||||| |||| ||| | || || |||| ||||||||
Db 201 CAAGGACAGCGCCTGGAGTGGATTGGGAGGATTTATCCTGGAAATGGTAATACTAAGTACAAT 260

Qy 241 GAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAG 300
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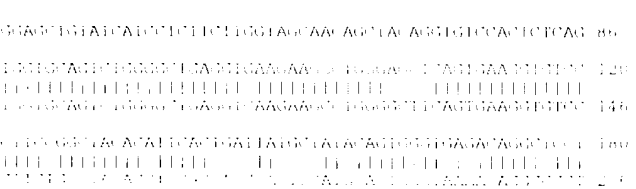
Qy 301 CTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTATGGTTAC 360
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Db 321 GACCTCACCAGCGAAGATGAGGCTGTCTATTACTGTGCAAGATCGACTATGGTTAC 380

Qy 361 GACGGGGGCTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA 409
||||| | || |||||||||||||||||||||||||||||||||||||||||||||
Db 381 TACGACGGGGGCTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA 440

RESULT 14
US 10-216-484-88
; Sequence 88, Application US/10216484
; Publication No. US2003018017A1
; GENERAL INFORMATION:
; APPLICANT: Sekikawa, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Imaki, Hideki
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti Fas Antibodies
; FILE REFERENCE: 9801/PCT/EP/BG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/054,599
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 88
; LENGTH: 2077
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Restored DNA
; OTHER INFORMATION: encoding the heavy chain of a humanized anti Fas
; OTHER INFORMATION: antibody
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (27)..(83)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (741)..(1131)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1177)..(1294)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1625)..(1721)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (27)..(740)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1132)..(1176)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1295)..(1624)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1722)..(2042)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (84)..(740)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1132)..(1176)
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; LOCATION: (1722)..(2042)
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; NAME/KEY: CDS
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; FEATURE:
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; LOCATION: (1132)..(1176)
; FEATURE:
; NAME/KEY: CDS
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1722)..(2042)
US 10-216-484-88

Query Match 61.4%; Score 248.8; DB 9; Length 2077;
Best Local Similarity 76.9%; Pred. No. 6e-71;
Matches 423; Conservative 0; Mismatches 82; Indels 15; Gaps 1;

QY 1 ATGGGGTCGAACTGTATCATCTTCTTCCTGGTTGCTGTTGCTACAGGTGTGCACTCCCAG 60
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RESULT 14
US-10-216-484-156
; Sequence 156, Application US/10216484
; Publication No. US20040109976A1
; GENERAL INFORMATION:
; APPLICANT: Seriewa, No. US20030104976A1ufusa
; APPLICANT: Hamuyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 09/475,744
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,503
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 159
; SEQ ID NO 156
; LENGTH: [illegible]
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (27)..(84)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (741)..(1131)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1177)..(1294)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1295)..(1725)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (27)..(740)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1132)..(1176)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1295)..(1624)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1722)..(2042)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (84)..(740)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1132)..(1176)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1295)..(1624)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1722)..(2042)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(740)
; FEATURE:
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; LOCATION: (1132)..(1176)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1295)..(1624)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1722)..(2042)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Isolated DNA
; OTHER INFORMATION: encoding the heavy chain of humanized anti Fas
; OTHER INFORMATION: antibody
US-10-216-484-156

Query Match 60.6%; Score 245.6; DB 9; Length 2077;
Best Local Similarity 76.1%; Pred. No. 5.7e-70;
Matches 321; Conservative 0; Mismatches 84; Indels 15; Gaps 1;

RESULT 15
US-10-233-996-47
; Sequence 47, Application US/10233996
; Publication No. US20040096976A1
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang Yull

```
;  APPLICANT:  Yeung, Simon Kwan
;  TITLE OF INVENTION: HUMANIZED ANTIBODIES LR-00503 AND LR-00506 SPECIFIC FOR HUMAN 4-1
;  TITLE OF INVENTION:  PHARMACEUTICAL COMPOSITIONS COMPRISING SAID HUMANIZED ANTIBODIES
;  FILE REFERENCE: 4994.0102P
;  CURRENT APPLICATION NUMBER: US/10/233,996
;  CURRENT FILING DATE:  2002-12-04
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
;  LENGTH: 423
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Gene coding
;  OTHER INFORMATION: for variable region of heavy chain of humanized
;  OTHER INFORMATION: antibody BJ484.2
US-09-249-011b-5.rnpb Seq 47

  Query Match             60.5%;  Score 245...;  DB 9;  Length 423;
  Best Local Similarity   76.6%;  Pred. No. 4.6e-20;
  Matches  ...;  Conservative    0;  Mismatches   88;  Indels    9;  Gaps    1;

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              ||| | ||||  || |||||||  |||| |||  | ||||||||||  ||| ||||||||| 
Db         10 ATGGGATGGAGCTATATCATCCTCTTTTTGGTAGCAACAGCTACAGATGTCCACTCCCAG 69

Qy         61 GTCCAGCTTGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTGTCC 120
              |||| ||||||||||||||||| |||||||||||||||  |||||||||||||||
Db         70 GTCCAATTGGTGCAGTCTGGGTCTGAGTTGAAGAAGCCTGGGGCCTCAGTGAAGGTGTCC 129

Qy        121 TGCAAGTCTTCCGGCTACACATTCACCGATTATGCTATACACTGGGTGAGACAGGCCCCT 180
              |||| |||| |||||||| |||      ||    || || ||||| | |||| |||
Db        130 TGCAAGGCTTCTGGATACACCTTCACCAGTTATGCTATGCATTGGGTGCGACAGGCCCCT 189

Qy        181 GGACAAGGGCTTGAGTGGATGGGATGGATCAACACCGAGACTGGTGAGCCAACATATGCA 240
              |||||  |||| |||||||| |||| ||||  |  | | | | ||| ||||| |
Db        190 GGACAAGCGCTTGAGTGGATGGGAGGATTAACACCGGAAATGGTGAGCCAACATATGCA 249

Qy        241 GATGACTTCAAGGGACGGTTTGCCTTCTCTTTGGAAACCTCTGCCAGCACTGCCTATTTG 300
              |||||||  |||    |  ||||| |||||||||| ||  ||||||||||| |||
Db        250 GATGACTTCAAGGGACGCTTTGACTTCTCTTTGGAAACCTCTGCCAGCACTGCCTATTTG 309

Qy        301 CAGATCAACAACCTCAAAAATGAGGACACGGCTACATATTTCTGTGCAAGA 351
              |||| ||  |||||||||||| |||| || |||||||||||| |||||
Db        310 CAGATCCACAACCTCAAAAATGAGGACATGGCTACATATTTCTGTGCAAGA 360

Qy        352 GGGGGTTCCGGCTACGACGGGGGCTTTGACTACTGGGGCCAAGGCACCACT 402
              |||| ||  | | ||||||||| |||| || || |||| |||| |||
Db        361 GGGGACTACGGTAGGGACGGGTTCTTTGACTACTGGGGCCAAGGCACCACT 411

Qy        403 CTCACA 408
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Db        412 CTCACA 417


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OM nucleic - protein search, using sw model

Run on: June 17, 2003, 13:08:03 ; Search time 34.382 Seconds
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Title: US-09-249-011B-5
Perfect score: 405
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153838381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

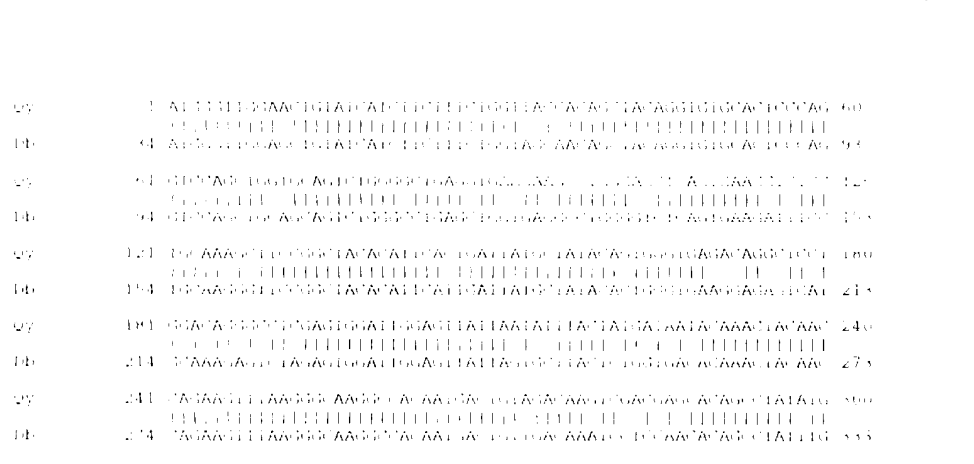
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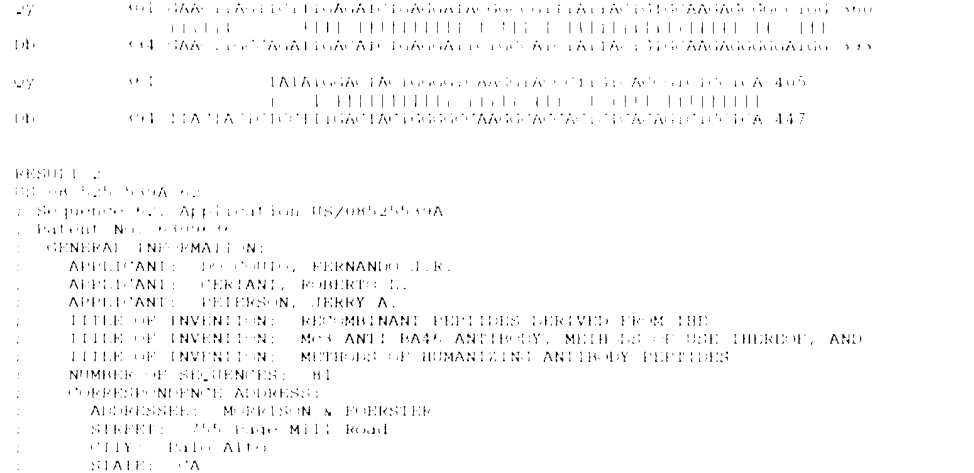
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2	251.4	62.0	434	4	US-08-525-539A-62	Sequence 62, Appl
3	250.6	62.0	451	4	US-08-576-378A-11	Sequence 11, Appl
4	250.6	62.0	451	5	PCT-US93-11612-11	Sequence 11, Appl
5	251.6	62.1	423	4	US-09-438-954-43	Sequence 43, Appl
6	248.2	61.3	433	1	US-08-147-117D-111	Sequence 111, App
7	247.2	61.0	433	1	US-08-436-717-111	Sequence 111, App
8	245.2	60.5	423	4	US-09-438-954-47	Sequence 47, Appl
9	245	60.5	405	1	US-07-634-278-68	Sequence 68, Appl
10	245	60.5	405	1	US-08-477-728-68	Sequence 68, Appl
11	245	60.5	405	1	US-08-474-040-68	Sequence 68, Appl
12	245	60.5	405	1	US-08-487-200-68	Sequence 68, Appl
13	245	60.5	405	4	US-08-484-547-68	Sequence 68, Appl
14	244.8	60.5	421	3	US-08-836-561-62	Sequence 62, Appl
15	240.6	59.4	433	1	US-07-634-278-18	Sequence 18, Appl
16	238.6	58.9	433	1	US-08-477-728-18	Sequence 18, Appl
17	238.6	58.9	433	1	US-08-474-040-18	Sequence 18, Appl
18	238.6	58.9	433	1	US-08-487-200-18	Sequence 18, Appl
19	238.6	58.9	433	4	US-08-484-547-18	Sequence 18, Appl
20	237.6	58.7	422	1	US-08-482-882-77	Sequence 77, Appl
21	237.6	58.7	422	1	US-08-483-389-77	Sequence 77, Appl
22	237.6	58.7	422	2	US-08-487-114D-77	Sequence 77, Appl
23	237.6	58.7	422	2	US-08-473-503-77	Sequence 77, Appl
24	237.6	58.7	422	2	US-08-483-932-77	Sequence 77, Appl
25	237.6	58.7	422	2	US-08-720-420A-77	Sequence 77, Appl
26	237.6	58.7	422	3	US-08-714-017-77	Sequence 77, Appl
27	237.6	58.7	422	3	US-08-475-688-77	Sequence 77, Appl
28	236.8	58.5	409	4	US-08-646-265A-98	Sequence 98, Appl
29	236	58.3	421	3	US-08-836-561-73	Sequence 73, Appl
30	234.4	57.9	421	3	US-08-836-561-77	Sequence 77, Appl
31	234	57.8	423	4	US-09-438-954-45	Sequence 45, Appl
32	233.6	57.7	408	5	PCT-US93-11611-5	Sequence 5, Appli
33	232.8	57.5	429	1	US-08-236-520-6	Sequence 6, Appli
34	232.8	57.5	429	5	PCT-US95-05262-6	Sequence 6, Appli
35	232.2	57.3	405	1	US-08-147-117D-26	Sequence 26, Appl
36	232.2	57.3	405	1	US-08-436-717-26	Sequence 26, Appl
37	231.4	57.1	461	2	US-07-916-098A-39	Sequence 39, Appl
38	231.4	57.1	2560	2	US-07-916-098A-44	Sequence 44, Appl
39	231	57.0	433	3	US-08-673-799C-99	Sequence 99, Appl
40	231	57.0	433	4	US-09-393-385B-99	Sequence 99, Appl
41	229.6	56.7	421	3	US-08-836-561-82	Sequence 82, Appl
42	229.4	56.6	432	2	US-08-483-528B-60	Sequence 60, Appl
43	229.4	56.6	432	3	US-08-673-799C-60	Sequence 60, Appl
44	229.4	56.6	432	4	US-09-393-385B-60	Sequence 60, Appl
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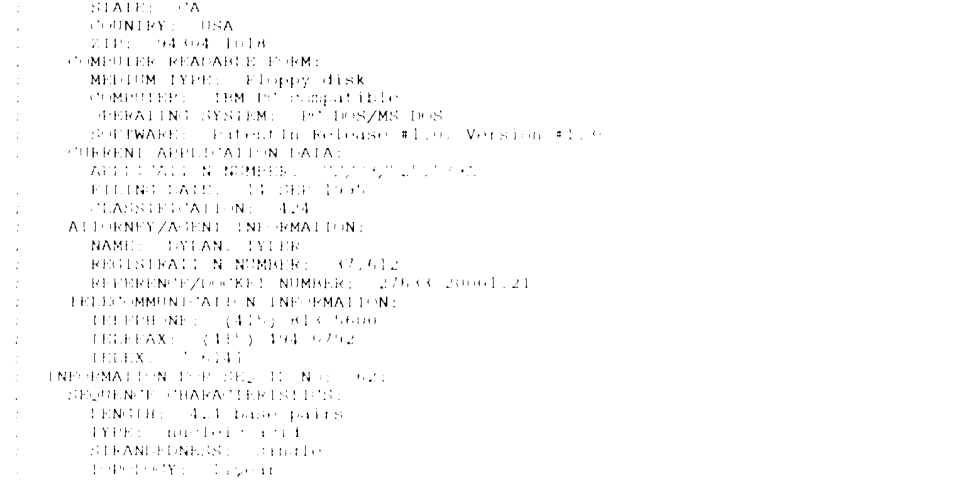
ALIGNMENTS

RESULT 1
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; Sequence 4, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDW CHAIN ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: [illegible]
; STREET: 1250 Connecticut Ave. NW Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; * APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: P011.0586.000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 524 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 34..522
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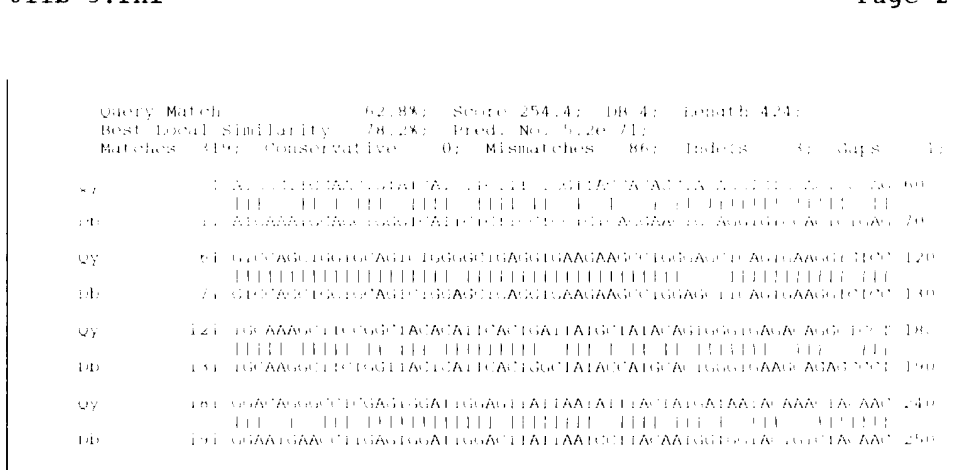
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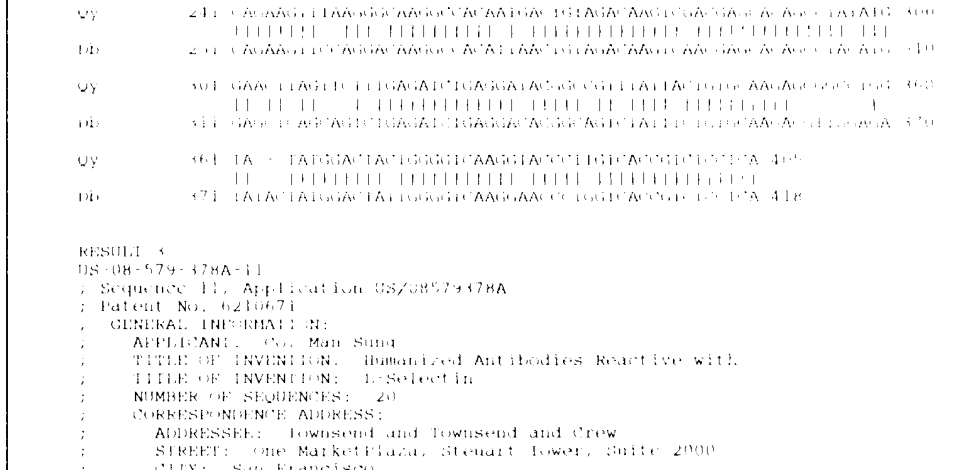


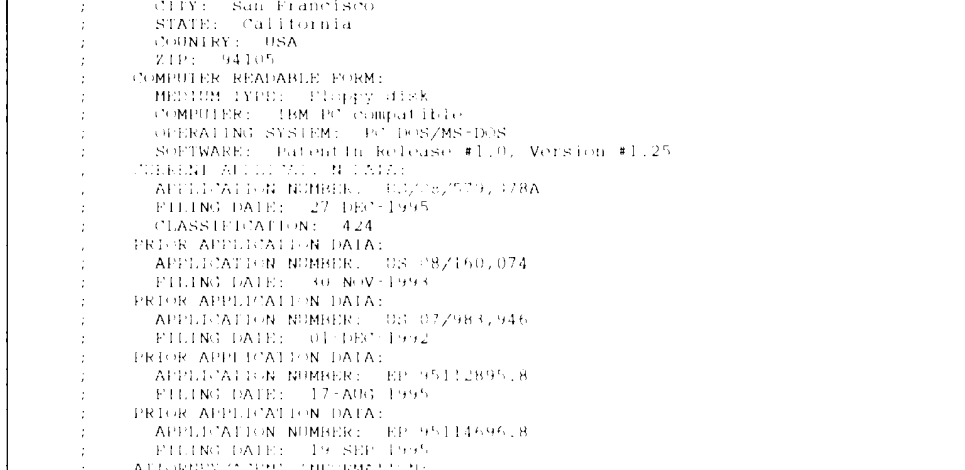




RESULT 2
US-08-525-569A-2
; Sequence 2, Application US/08525569A
; Patent No. 5699798
; GENERAL INFORMATION:
; APPLICANT: [illegible], FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM IBE
; TITLE OF INVENTION: MC8 ANTI BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: [illegible]
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633.20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
RESULT 2
US-08-525-569A-2







RESULT 3
US-08-579-878A-11
; Sequence 11, Application US/08579878A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Wu, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/579,878A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Tiefenschnitz, Joe G.

```
;       REGISTRATION NUMBER:  37,505
;       REFERENCE/DOCKET NUMBER:  11823-0222P
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415 326 2422
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  451 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  12..431
US-08-478A-11

  Query Match             62.6%;  Score 253.6;  DB 4;  Length 451;
  Best Local Similarity   77.6%;  Pred. No. 9.5e-71;
  Matches  326;  Conservative    0;  Mismatches   79;  Indels   15;  Gaps    1;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTAGCACAGCTACAGGTGTCCACTCCCAG 60
              |||||| |||| |||||||||| |||| |||| | ||||||||| |||| |||||||||
Db         12 ATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGTGTCCACTCCCAG 71

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 120
              ||||||||||| |||||||| |||| || |||| |||||||||.|||||||||| ||
Db         72 GTCCAGTCGGTACAGTCTGGAGCTGAAGTCAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 131

Qy        121 TGCAAAGTTTCCGGCTACACATTCACTGATTATGCTATACATTGGGTGAAGCAGGCTCCT 180
              |||| |||| || |||||||||||   |||| || || |||||||||||||||||| ||
Db        132 TGCAAGGCTTCTGGATACACATTCACTAGCTATGTTATGCATTGGGTGAAGCAGGCCCCT 191

Qy        181 GGACAGGGGCTTGAGTGGATTGGATGGATTAATACTTACTATGGAAATAAATATAATGAG 240
              || || || ||||||||||||||   |||| ||  |||| |||||  ||| || ||||
Db        192 GGTCAAGGACTTGAGTGGATGGGATGGATTAACACCTACAATGGAGTGCCAACGTACAAT 251

Qy        241 AAGAAGTTCAAGGGCAAAGTCACAATGACTACAGACACATCCACGAGCACAGCCTACATGG 300
              |||||| || |||   | |||||| ||| ||||  |||| |||| || | ||||||| |||
Db        252 GAGAACTTCAAAAACAGAGTCACGTTAACTACGGACACATCCACGAGCACAGCCTACATGG 311

Qy        301 GAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCAAGATCGGATC--- 358
              |||||| ||    ||| |||| |||||| | || || ||||||||||||||| | ||  |
Db        312 GAACTGAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCAAGATCGGTTTAT 371

Qy        359 ---------GGTATATGGACTATTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 403
                        |||| | ||   |||||| ||||||| || |||| ||||||||||
Db        372 GTAGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA 414

RESULT 4
PCT/US94/11612-11
; Sequence 11, Application PC/PCT/US94/11612
; GENERAL INFORMATION:
;   APPLICANT:  Co, Man Sung
;   TITLE OF INVENTION:  Humanized Antibodies Reactive with
;   TITLE OF INVENTION:  L-Selectin
;   NUMBER OF SEQUENCES:  12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Townsend and Townsend Khourie and Crew
;     STREET:  One Market Plaza, Steuart Tower, Suite 2000
;     CITY:  San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94105
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US94/11612
;     FILING DATE:
;       CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/983,946
;     FILING DATE:  01-DEC-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Smith, William M.
;     REGISTRATION NUMBER:  30,223
;     REFERENCE/DOCKET NUMBER:  11823-22
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415-326-2403
;     TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  451 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  12..431
PCT-US94-11612-11

  Query Match             62.6%;  Score 253.6;  DB 5;  Length 451;
  Best Local Similarity   77.6%;  Pred. No. 9.5e-71;
  Matches  326;  Conservative    0;  Mismatches   79;  Indels   15;  Gaps    1;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTAGCACAGCTACAGGTGTCCACTCCCAG 60
              |||||| |||| |||||||||| |||| |||| | ||||||||| |||| |||||||||
Db         12 ATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGTGTCCACTCCCAG 71

Qy         61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 120
              ||||||||||| |||||||| |||| || |||| |||||||||.|||||||||| ||
Db         72 GTCCAGTCGGTACAGTCTGGAGCTGAAGTCAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 131

Qy        121 TGCAAAGTTTCCGGCTACACATTCACTGATTATGCTATACATTGGGTGAAGCAGGCTCCT 180
              |||| |||| || |||||||||||   |||| || || |||||||||||||||||| ||
Db        132 TGCAAGGCTTCTGGATACACATTCACTAGCTATGTTATGCATTGGGTGAAGCAGGCCCCT 191

Qy        181 GGACAGGGGCTTGAGTGGATTGGATGGATTAATACTTACTATGGAAATAAATATAATGAG 240
              || || || ||||||||||||||   |||| ||  |||| |||||  ||| || ||||
Db        192 GGTCAAGGACTTGAGTGGATGGGATGGATTAACACCTACAATGGAGTGCCAACGTACAAT 251

Qy        241 AAGAAGTTCAAGGGCAAAGTCACAATGACTACAGACACATCCACGAGCACAGCCTACATGG 300
              |||||| || |||   | |||||| ||| ||||  |||| |||| || | ||||||| |||
Db        252 GAGAACTTCAAAAACAGAGTCACGTTAACTACGGACACATCCACGAGCACAGCCTACATGG 311

Qy        301 GAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCAAGATCGGATC--- 358
              |||||| ||    ||| |||| |||||| | || || ||||||||||||||| | ||  |
Db        312 GAACTGAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCAAGATCGGTTTAT 371

Qy        359 ---------GGTATATGGACTATTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 403
                        |||| | ||   |||||| ||||||| || |||| ||||||||||
Db        372 GTAGCTTACTGGGGCCAAGGGACTCTGGTCACCGTCTCCTCA 414

RESULT 5
US-09-438-954-43
; Sequence 43, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
;  APPLICANT: BONG, Hyo Jeong
;  APPLICANT: PARK, Sung Sup
;  APPLICANT: KANG, Young Jun
;  APPLICANT: KANG, Chang Yull
;  APPLICANT: YOON, Sung Kwan
;  TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN E-SELECTIN AND
;  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME
;  FILE REFERENCE: P98-1240
;  CURRENT APPLICATION NUMBER: US/09/438,954
;  CURRENT FILING DATE: 1999-11-12
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 13
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene coding
; OTHER INFORMATION: for variable region of heavy chain of humanized
; OTHER INFORMATION: antibody HZ4B4 I
US-09-438-954-13

Query Match 92.1%; Score 2516; DB 4; Length 425;
Best Local Similarity 77.9%; Pred. No. 1e-77;
Matches 621; Conservative 0; Mismatches 84; Indels 9; Gaps 1;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTAGCAGCTACAGGTGTGCACTCCCAG 60
Db 10 ATGGGATGGAGCTATATCATCCTCTTTTGGTTACAACAGCTACAGATGTCCACTCCCAG 69

Qy 61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 120
Db 70 GTCCAGCTTCTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 129

Qy 121 TGCAAAGCATCTGGCTACACCTTCACTGATTATGCTATACACTGGGTGAAGCAGGCCCCT 180
Db 130 TGCAAGGCTTCTGGATACACCTTCACAA---ATATGCTATACACTGGGTGAAGCAGGCCCCT 186

Qy 181 GGACAAGGGCTTGAGTGGATTGGATGGATTAACACTGAGACTGGTGAGCCAACATATGCA 240
Db 187 GGACAAGGTCTTGAGTGGATTGGATGGATTAACACTAAA---ACTGGTGAGCCAACATATGCA 243

Qy 241 GATGACTTCAAGGGACGGTTTGCCTTCTCTTTGGAAACCTCTGCCAGCACTGCCTATTTG 300
Db 244 GATGACTTCAAGGGACGGTTTGCCTTCTCTTTGGAAACCTCTGCCAGCACTGCCTATTTG 303

Qy 301 CAGATCAACAACCTCAAAAATGAGGACACGGCTACATATTTCTGTGCAAGAT---- 351
Db 304 CAGATCAACAACCTCAAAAATGAGGACATGGCTACATATTTCTGTGCAAGATCTTTACT 360

Qy 352 GTTGGTACTGGTATATGGCACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
Db 361 GTTGGTACTGGTATATGGCACTACTGGGGCCAAGGTACCCTTGTCACCGTCTCCTCA 414

RESULT 6
US-08-147-112D-111
; Sequence 111, Application US/08147112D
; Patent No. 5712367
; GENERAL INFORMATION:
; APPLICANT: ISHIDEYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RECHAINED HUMAN ANTIBODY I- HUMAN
; TITLE OF INVENTION: INTERLEUKIN 8 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 815 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-4102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSEQ for Windows Release #1.0, Version #1.50
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,112D
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,200
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 5400/320/AAE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..420
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 16..420
US-08-147-112D-111

Query Match 91.5%; Score 2482; DB 1; Length 433;
Best Local Similarity 75.8%; Pred. No. 4.7e-69;
Matches 607; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 ATGGGTTGGAACTGTATCATCTTCTTCTGGTTAGCAGCTACAGGTGTGCACTCCCAG 60
Db 16 ATGGGATGGAGCTGGAGGGTCTTCTTCTTGGCTGGCTGTAGCTCCCAGGTGCTCACTCCCAG 75

Qy 61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 120
Db 76 GTCCAGCTTCTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 135

Qy 121 TGCAAAGCATCTGGCTACACCTTCACTGATTATGCTATACACTGGGTGAAGCAGGCCCCT 180
Db 136 TGCAAGGCTTCTGGATACACCTTCACAAATATGCTATACACTGGGTGAAGCAGGCCCCT 195

Qy 181 GGACAAGGGCTTGAGTGGATTGGATGGATTAACACTGAGACTGGTGAGCCAACATATGCA 240
Db 196 GGACAAGGTCTTGAGTGGATTGGATGGATTAACACTAAAACTGGTGAGCCAACATATGCA 255

Qy 241 GATGACTTCAAGGGACGGTTTGCCTTCTCTTTGGAAACCTCTGCCAGCACTGCCTATTTG 300
Db 256 GATGACTTCAAGGGCAGGTTCGCCTTCTCTTTGGAAACCTCTGCCAGCACTGCCTATTTG 315

Qy 301 CAGATCAACAACCTCAAAAATGAGGACACGGCTACATATTTCTGTGCAAGATCTTTACT 360
Db 316 CAGATCAGCAACCTCAAGAATGAGGACATGGCTACATATTTCTGTGCAAGATCTTTACT 375

Qy 361 TATATGGCACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
Db 376 CTGTTGGTTACTGGTACGCAAGGAACCCTGGTCACCGTCTCCTCA 420

RESULT 7
US-08-436-717-111
; Sequence 111, Application US/08436717
; Patent No. 5817793
; GENERAL INFORMATION:
; APPLICANT: ISHIDEYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose

```
;     TITLE OF INVENTION:  RECOMBINANT HUMAN ANTIBODY TO HUMAN
;     TITLE OF INVENTION:  INTERLEUKIN 6 ASSAY
;     NUMBER OF SEQUENCES:  158
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  3000 K Street, N.W., Suite 500
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/476,737
;       FILING DATE:
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/137,317
;       FILING DATE:  20-DEC-1993
;       APPLICATION NUMBER:  WO PCT/JP92/00544
;       FILING DATE:  24-APR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 3 92081
;       FILING DATE:  19-FEB-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 3 95476
;       FILING DATE:  25-APR-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WEGNER, Harold C.
;       REGISTRATION NUMBER:  25,258
;       REFERENCE/DOCKET NUMBER:  [illegible]/AA-E
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  111:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  433 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..420
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  1..420
US-08-476-717-111

  Query Match             61.8%;  Score 248.2;  DB 1;  Length 433;
  Best Local Similarity   75.8%;  Pred. No. 4.7e-69;
  Matches  307;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTCTTGGTTACTACAGCTACAGGTGTCCACTCCCAG 60
              ||||  |||| ||| |  ||||||  ||| | |   |||| ||||||  ||||||||||
Db         16 ATGGACTTGGACTGGAGGGTCTTCTTCTTGCTGGCTGTAGCTACAGGTGTCCACTCCCAG 75

Qy         61 GTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATGTCCTGC 120
              ||  |||| |||:|||||| ||||||||||||||||||||||  ||||||||||| |||
Db         76 GTGCAGCTTCAGCAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGTTGTCCTGC 135

Qy        121 AAAGCTTCTGGATACACATTCACTGACTACTATATAAACTGGGTGAAGCAGAGGCCTGGA 180
              |||||  |||| || ||| ||||||||  ||||  |||| |||||| | |||| ||
Db        136 AAAGGCTCTGGGTACACCTTCACTAGCTACTATATACACTGGGTGCGCCAGGCCCCTGGA 195

Qy        181 CAAGGGCTTGAGTGGATTGGAGAGATTAATCCTAGCAACGGTCGTACTAACTACAATGAG 240
              |||||  | || |||||||| ||  |||| | || | ||| |  ||| | ||| ||
Db        196 CAAGCGACTGATTGGATGGGGTGTATTAATCCTGGCAACGATGATACTAAGTACAGTGAG 255

Qy        241 AAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 300
```

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                ||||||| |||||| | ||| || || |||| | |  |||||||||||||| |||
Db        256 AAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 315

Qy        301 GAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCG 355
              || || ||   | |||||||||| || |||| ||  |||||||||| |||| ||
Db        316 GAGCTCAGCAGCCTGAGGTCTGAGGACACTGCCGTCTATTACTGTGCAAGATCG 370

Qy        356 ATTACGACGGGGGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 415
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ATTACGACGGGGGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 430

Qy        416 GCC 418
              |||
Db        431 GCC 433


RESULT 8
US-09-438-954-47
; Sequence 47, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
;  APPLICANT: BANG, Hyo Jeong
;  APPLICANT: PARK, Sung Sup
;  APPLICANT: KANG, Young Jun
;  APPLICANT: KANG, Chang-Yull
;  APPLICANT: YOON, Sung Kwan
;  TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN IL-6 AND
;  TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME
;  FILE REFERENCE: 1303-124P
;  CURRENT APPLICATION NUMBER: US/09/438,954
;  CURRENT FILING DATE: 1999-11-12
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
;  LENGTH: 423
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Gene coding
;  OTHER INFORMATION: for variable region of heavy chain of humanized
;  OTHER INFORMATION: antibody HP4P4-2
US-09-438-954-47

  Query Match             60.1%;  Score 245.2;  DB 4;  Length 423;
  Best Local Similarity   75.6%;  Pred. No. 4.1e-68;
  Matches  317;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    1;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTCTTGGTTACTACAGCTACAGGTGTCCACTCCCAG 60
              ||||  |||| ||| |  ||||||  ||| | |   |||| ||||||  ||||||||||
Db         16 ATGGACTTGGACTGGAGGGTCTTCTTCTTGCTGGCTGTAGCTACAGGTGTCCACTCCCAG 75

Qy         61 GTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATGTCCTGC 120
              ||||| |||||||||||||||||||||||||||||||||||||  |||| |||| |||
Db         76 GTCCAACTGCAGCAGTCTGGGGCTGAAGTGAAGAAGCCTGGGGCCTCAGTGAAGGTGTCCTGC 135

Qy        121 TGCAAAGCTTCTGGATACACATTCACTGACTACTATATAAACTGGGTGAAGCAGAGGCCTGGA 180
              |||||  |||| ||| ||||||||  ||||  |||| |||||| | |||| ||
Db        136 TGCAAGGCTTCTGGGTACACCTTCACTAGCTACTATATACACTGGGTGCGCCAGGCCCCTGGA 195

Qy        181 CAAGGGCTTGAGTGGATTGGAGAGATTAATCCTAGCAACGGTCGTACTAACTACAATGAG 240
              |||||  | || |||||||| ||  |||| | || | ||| |  ||| | ||| ||
Db        196 CAAGCGACTGATTGGATGGGGTGTATTAATCCTGGCAACGATGATACTAAGTACAGTGAG 255

Qy        241 AAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 300
              |||||||| |||||| | ||| || || |||| | |  |||||||||||||| |||
Db        256 AAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 315

Qy        301 GAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCG 355
              || || ||   | |||||||||| || |||| ||  |||||||||| |||| ||
Db        316 GAGCTCAGCAGCCTGAGGTCTGAGGACACTGCCGTCTATTACTGTGCAAGATCG 370

Qy        356 ATTACGACGGGGGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 415
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ATTACGACGGGGGCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 430

Qy        416 GCC 418
              |||
Db        431 GCC 433


RESULT 9
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US-07-634-278-68
; Sequence 68, Application US/07634278
; Patent No. 5580849
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  Co, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  QUELLING, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBULINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28 SEP 1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13 FEB 1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326 2400
;      TELEFAX:  (415) 326 2422
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  405 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..405
US-07-634-278-68

  Query Match             99.5%;  Score 245;  DB 1;  Length 405;
  Best Local Similarity   99.3%;  Pred. No. 4.7e-68;
  Matches  405;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTCCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
              ||||| ||| ||| ||| | |||| || | |  | || |||| || ||||  ||
Db          1 ATGGCATGGAGCTGGATCTTTCTCTTCCTCCTGTCAGGAACTGCAGGTGTCCACTCTGAG 60

Qy         61 GTCCAGCTGCAGCAGTCTGGGGCTGAGCTGGAAAAGCCTGGGGCCTCAGTGAAGATATCC 120
              |||||||  |||||| || ||||| || |||| |||| | ||||| | |||||||||| |
Db         61 GTCGAGCTTCAGGAGTCAGGACCTGAGCTGGTGAAGCCTTCTCAGACTCTGTCCCTCACC 120

Qy        121 TGCACTGTCACTGGCTACTCAATCACCAGTGATTATGCCTGGAACTGGATCCGGCAGTTT 180
              |||| |||| || |||||||||||| |  | || || |||| |  ||| |  ||
Db        121 TGCAGCGTCACTGGCTACTCCATCACCAGTGGTTATGCCTGGCACTGGATCCGGCAGTTC 180

Qy        181 CCAGGAAACAAACTGGAGTGGATGGGATACATAACTTACAGTGGTAGCACTGGCTACAAC 240
              |||||||| ||| |||||||||| |||||||||||| || | |||||||||| |||
Db        181 CCAGGAAAGAAGCTTGAGTGGATTGGATATATTTATCCTTACAATGGTGGTACTGGCTACAAC 240

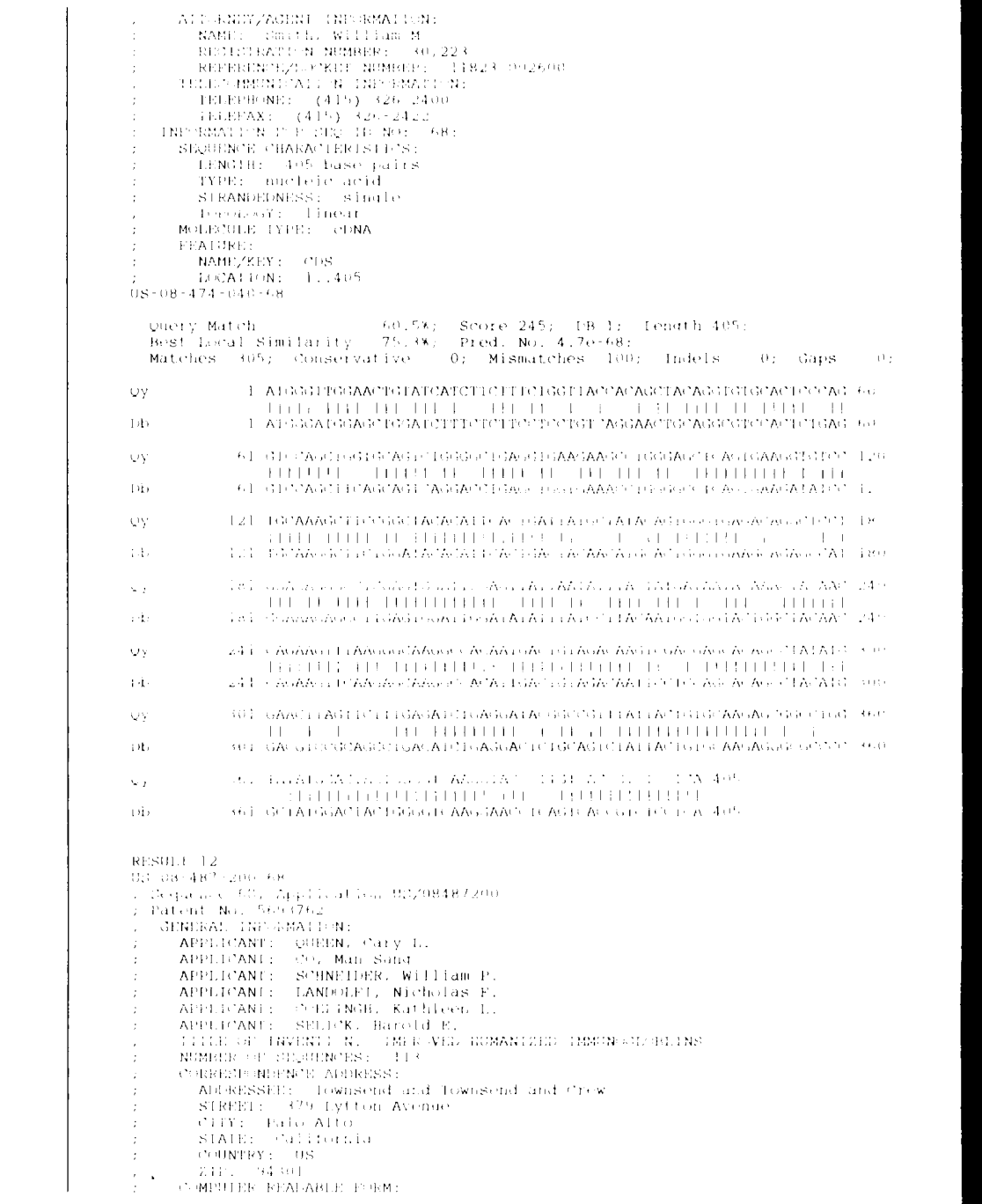
Qy        241 CAGAAGTTCAAGGGCAAGGCCACAATGACTGTAGACAAGTCGAGCAGCACAGCCTATATG 300
              |||||||| ||| |||||||||| |||||||||||| || | ||||||||||| |||
Db        241 CAGAAGTTCAAGGAGAAGGCCACATTGACTGTAGACAAATCCAGCAGCACAGCCTACATG 300

Qy        301 GAACTTAGTTCCTTGACATCTGAGGATACTGCCGTTTATTACTGTGCAAGAGGGGGCTGT 360
              || | | |    ||| |||||||| | || || |||||||||||||| | | |
Db        301 GACGTGCGCAGCCTGACAATCGAGGACTCTGCAGTCTATTAC[GT]CAAGACGCGCCGCT 360

Qy        361 TATAGGACTACTGGGGCCAAGGCACCCTTGTCACCGTCTCCTCA 405
              |||||||||||||||||||| |||  |||||||||||||
Db        361 GCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 405


RESULT 10
US-08-477-728-68
; Sequence 68, Application US/08477728
; Patent No. 5580849
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBULINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,728
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28 SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13 FEB 1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28 DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326 2400
;      TELEFAX:  (415) 326 2422
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  405 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..405
US-08-477-728-68
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Query Match 60.5%; Score 245; DB 1; Length 405;
Best Local Similarity 75.3%; Pred. No. 4.7e-68;
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;



RESULT 11
US-08-474-040-68
; Sequence 68, Application US/08474040
; Patent No. 5990276
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/631,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..405
US-08-474-040-68

Query Match 60.5%; Score 245; DB 1; Length 405;
Best Local Similarity 75.3%; Pred. No. 4.7e-68;
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

RESULT 12
US-08-487-200-68
; Sequence 68, Application US/08487200
; Patent No. 5990762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: Co, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:

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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC DOS/MS DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/484,537
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/634,278
;       FILING DATE:  19 DEC 1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/590,274
;       FILING DATE:  28 SEP 1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/310,252
;       FILING DATE:  13 FEB 1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/290,975
;       FILING DATE:  28 DEC 1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William M
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  11823-002610
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 326 2400
;       TELEFAX:  (415) 326 2422
;   INFORMATION FOR SEQ ID NO:  68:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  405 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..405
US-08-484,537-68

  Query Match             60.5%;  Score 245;  DB 4;  Length 405;
  Best Local Similarity   75.4%;  Pred. No. 4.7e-68;
  Matches  305;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTCCTGGTTACTACAGGTACAGGTGTCCACTCCCAG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGATGGAGCTGGATCTTTCTCTTCCTGGTTACAGGAACCTGCAGCAGTGGTGTCCAG 60

Qy         61 GTTCAGTTGCAGCAGTCTGGGGCTGAGCTTGAACAAGCCTGGGGCTCAGTCAAGTTGTCC 120
              |||||||||  ||||||| ||  |||||||| ||  |||||||||  |||||||||| ||||
Db         61 GTCCAGGTCCAGCAGCCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCC 120

Qy        121 TGCAAAGCTTCTGGCTACACATTCACTGATTATTATATAAGTTGGGTGAAACAGAGGCCTGT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCAAGGCTTCTGGATACACATTCACTAGCTATTATATAAGTTGGGTGAAACAGAGGCCTGT 180

Qy        181 GGACAGGGCCTTGAGTGGATTGGATGGATTAATATTTACTATGGAAATACTAACTACAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGAAAGGGCCTTGAGTGGATTGGATGGATTAATATTTACTATGGAAATACTAACTACAAC 240

Qy        241 GAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 300
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Db        241 GAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 300

Qy        301 GAACTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGGGCCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAACTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGGGCCGC 360

Qy        361 TATGATGGTAGTAGGGGTTTCGATGTCTGGGGCACAGGGACCACGGTCACCGTCTCCTCA 405
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATGATGGTAGTAGGGGTTTCGATGTCTGGGGCACAGGGACCACGGTCACCGTCTCCTCA 405

RESULT 10
US-08-484,537-68
; Sequence 68, Application US/08484537
; Patent No. 6180370
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  Co, Mae Suna
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  CHELLINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBULINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/484,537
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326 2422
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  405 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..405
US-08-484,537-68

  Query Match             60.5%;  Score 245;  DB 4;  Length 405;
  Best Local Similarity   75.4%;  Pred. No. 4.7e-68;
  Matches  305;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTCCTGGTTACTACAGGTACAGGTGTCCACTCCCAG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGATGGAGCTGGATCTTTCTCTTCCTGGTTACAGGAACCTGCAGCAGTGGTGTCCAG 60

Qy         61 GTTCAGTTGCAGCAGTCTGGGGCTGAGCTTGAACAAGCCTGGGGCTCAGTCAAGTTGTCC 120
              |||||||||  ||||||| ||  |||||||| ||  |||||||||  |||||||||| ||||
Db         61 GTCCAGGTCCAGCAGCCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCC 120

Qy        121 TGCAAAGCTTCTGGCTACACATTCACTGATTATTATATAAGTTGGGTGAAACAGAGGCCTGT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCAAGGCTTCTGGATACACATTCACTAGCTATTATATAAGTTGGGTGAAACAGAGGCCTGT 180

Qy        181 GGACAGGGCCTTGAGTGGATTGGATGGATTAATATTTACTATGGAAATACTAACTACAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGAAAGGGCCTTGAGTGGATTGGATGGATTAATATTTACTATGGAAATACTAACTACAAC 240

Qy        241 GAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 300

Qy        301 GAACTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGGGCCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAACTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGGGCCGC 360

Qy        361 TATGATGGTAGTAGGGGTTTCGATGTCTGGGGCACAGGGACCACGGTCACCGTCTCCTCA 405
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATGATGGTAGTAGGGGTTTCGATGTCTGGGGCACAGGGACCACGGTCACCGTCTCCTCA 405
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Qy          181 GGACAGGGCCTGGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 GGACAGGGCCTGGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240

Qy          241 CAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCGAGCACAGCCTATATG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 CAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCGTCCACAGCACAGCTACATG 300

Qy          301 GAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGGGGCCTGG 360
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 GACGTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGAGGGCGCCCC 360

Qy          361 TATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCA 405
                |||||||||||||||||||||||||||||||||||||||||||||
Db          361 TCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 405


RESULT 14
US-09-838-961-62
; Sequence 62, Application US/09838961
; Patent No. 7078254
; GENERAL INFORMATION:
;     APPLICANT: KOIKE, Masamichi
;     APPLICANT: FUKUYA, Akiko
;     APPLICANT: NAKAMURA, Kazuyasu
;     APPLICANT: ITA, Akihiro
;     APPLICANT: ANAZAWA, Hidoharu
;     APPLICANT: HANAI, Noboru
;     APPLICANT: TAKAISO, Kiyoshi
;     TITLE OF INVENTION: Antibody Against Human Interleukin 5
;     TITLE OF INVENTION: Receptor Alpha Chain
;     NUMBER OF SEQUENCES: 106
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Fennie & Edmonds LLP
;       STREET: 1155 Avenue of the Americas
;       CITY: New York
;       STATE: NY
;       COUNTRY: USA
;       ZIP: 10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/838,961
;       FILING DATE: 09-MAY-1997
;       CLASSIFICATION: 424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: JP 8-272424
;       FILING DATE: 11-SEP-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Lawrence, III, Stanton T.
;       REGISTRATION NUMBER: 25,736
;       REFERENCE/DOCKET NUMBER: 7305.117-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 212-790-9090
;       TELEFAX: 212 869-9741
;       TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 62:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 421 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: other
US-09-838-961-62

  Query Match          94.5%;  Score 749.8;  DB 3;  Length 421;
  Best Local Similarity   75.7%;  Pred. No. 1e-66;
  Matches  314;  Conservative   93;  Mismatches   87;  Indels   15;  Gaps    1;

Qy            1 ATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTCCCAG 60
                |||| |||| || || | ||||||| | | | || ||||||| |||| ||
Db            1 ATGGAATGGAGTTGGATATTTCTCTTTCTCCTGTCAGGAACTGCAGGTGTCCACTCTGAG 60

Qy           61 GTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTGTCC 120
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 GTCCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCC 120

Qy          121 TGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACACTGGGTGCGACAGGCCCCT 180
                |||| |||| || |||||||||||  |||| ||| || |||||| ||||||| |||
Db          121 TGCAAGGCTTCTGGATACACATTCACTAGTTATGTTATTCACTGGGTGCGACAGGCCCCT 180

Qy          181 GGACAGGGCCTGGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACAAC 240
                || |||||||| |||||||| ||  |||||||  |||| ||||   || || |||||
Db          181 GGTCAGGGCCTTGAGTGGATAGGATATATTAATCCTTACAATGATGGTACTAAGTACAAT 240

Qy          241 CAGAAGTTCAAGGGCAAGGCCACAATGACTGTAGACAAGTCGAGCACAGCCTATATG 300
                ||| ||| |||| | |||||| |||| |||| ||| ||||||||||||| |||
Db          241 GAGAGGTTCAAAGGCAGAGTCACATTCACTGCAGACACATCCACGAGCACAGCCTACATG 300

Qy          301 GAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAG          345
                || || |||||  |||||||||||||| |||| |||| || ||||||||||| ||||
Db          301 GAGCTGAGGAGCCTGACATCTGACGACTCTGCGGTCTATTACTGTGCAAGAGAAGAATT 360

Qy          346 - - - ---GGACTGGCTATATGGACTACTGGGGTCAAGGAACCCTCGTCACCGTCTCCTCA 405
                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 AGGTACTATGGTCTACTGGGACGACTACTTCGACGTCTGGGGCACAAGGACCACGGTCACCGTCTCCTCA 420


RESULT 15
US-07-664-278-18
; Sequence 18, Application US/07664278
; Patent No. 5530101
; GENERAL INFORMATION:
;     APPLICANT: QUEEN, Cary L.
;     APPLICANT: CO, Man Sung
;     APPLICANT: SCHNEIDER, William P.
;     APPLICANT: LANDOLFI, Nicholas F.
;     APPLICANT: OSELLINO, Kathleen L.
;     APPLICANT: SELSING, Harold E.
;     TITLE OF INVENTION: IMMUNOGLOBULIN VARIABLE DOMAIN
;     NUMBER OF SEQUENCES: 114
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Townsend and Townsend Khourie and Crew
;       STREET: 379 Lytton Avenue
;       CITY: Palo Alto
;       STATE: California
;       COUNTRY: US
;       ZIP: 94301
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US 07/664,278
;       FILING DATE: 19-DEC-1990
;       CLASSIFICATION: 424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/559,274
;       FILING DATE: 28-SEP-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/310,252
;       FILING DATE: 13-FEB-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/290,079
;       FILING DATE: 28-DEC-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Smith, William M
;       REGISTRATION NUMBER: 30,223
;       REFERENCE/DOCKET NUMBER: 10825-002600
;     TELECOMMUNICATION INFORMATION
;       TELEPHONE: (415) 326-2400
```

```
;       TELEFAX:  (415) 426 2422
;   INFORMATION FOR SEQ ID NO:  18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  433 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
;     HYPOTHETICAL:  NO
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  6..431
;       OTHER INFORMATION:  /product= "Humanized anti-tac heavy
;       OTHER INFORMATION:  chain variable region, Seq ID. 18"
03 07 634 278 18

  Query Match:          98.9%;  Score 298.5;  DB 1;  Length 433;
  Best Local Similarity:   74.4%;  Pred. No. 5.1e-66;
  Matches  307;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTGGAACTGTATCATCTTCTTCCTGGTTGCAGCAGCTACAGGTGTCCACTCCCAG 60
              |||| |||| ||| ||| | |||| || | |     | | || ||||||| |||
Db          6 ATGGGATGGAGCTGGATCTTTCTCTTCCTCTCA GGTACAGGTGCAGCTGGTGGAGTCTGGG 65

Qy         61 GTCTATGTCAGTGGTGCAGCTGGGGGCTGAGGTGAAGAAGCCTGGGACCTCAGTGAAGGTCTCC 120
              |||||| || ||||||||||||||| || |||| |||||       ||||||| |||
Db         66 GGCTAGCTTGTCAGTCTGGGACTGAGCTAAGAAACCTGGGTCCTCAGTGAAGGTCTCC 125

Qy        121 TGCAAGGCTTCTGGCTACACATTCACTAGCTATGCTATAAGCTGGGTGCGACAGGCCCCT 180
              ||| | || || |||||||| || ||| || || || |||| || |||| |||
Db        126 TGCAAGGCTTCTGGCTACACCTTTACTAGCTACAGGATGCACTGGGTAAGGCAGGCCCCT 185

Qy        181 GGACAAGGGCTTGAGTGGATGGGATGGATCAACACCTACACTGGAGAGCCAACATATGCT 240
              |||||||| || || |||||||||  |||||||   |    ||   |||| | ||||
Db        186 GGACAAGGGCTTGAATGGATGGGATGGATCAACGCCGACACTGGCGAGACCACATATGCT 245

Qy        241 GCAGACTTCAAGGGCCGGTTCACCTTCTCCTTGGACACCTCTGCCAGCACAGCCTATCTG 300
              |||||| |||| |||||| |||| |||| ||| | || || |  |||||||| |||
Db        246 GCAGACTTCAAGGGACGGTTTACCTTCTCCTTGGAAACCTCTGCCAGCACAGCCTATCTG 305

Qy        301 GAAATTAGCAGCCTGAGAAATGAGGACACGGCTGTCTATTACTGTGCAAGAGGGGGCCTGG 360
              |||| ||     |||||||||||||| || || || ||||||||||||||| ||   ||
Db        306 GAAGTGAAGAGCCTGAGAATCGACGACACCGCAGTCTATTACTGTGCAAGAGGGGGCGGGG 365

Qy        361 TATAGCTACTACGGGGGCATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA 420
              | ||||||| |||||||||| |||| |||| |||| ||||||||
Db        366 GTCTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCA 410


Search completed: June 17, 2003, 20:00:42
Job time : 35.362 secs
```

GenCore version 5.1.6
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SW protein - protein search, using sw model

Run on: June 14, 2003, 15:02:48 ; Search time 14.1573 Seconds
(without alignments)
916.710 Million cell updates/sec

Title: US-09-249-011b-6
Perfect score: 520
Sequence: 1 MGWRCIIFFLVTTATGVHS.....AKAAWYMDVWGAGTLVTVSS 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96184422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	514.5	71.5	160	2	PL0105	anti-PR2 erythrocy
2	513.5	71.3	136	1	HVMSB1	Ig heavy chain pro
3	512.5	71.2	138	2	E32513	Ig heavy chain pro
4	512	71.1	135	2	S49530	anti-Sm antibody V
5	510	70.8	135	2	A30577	Ig heavy chain pro
6	501	69.6	139	1	MHMS18	Ig heavy chain pro
7	500	69.4	139	2	A27499	Ig heavy chain pro
8	498	69.2	141	2	JL0076	Ig heavy chain pro
9	494.5	68.7	131	2	A27494	Ig heavy chain V r
10	494.5	68.7	627	2	S14683	Ig mu chain precur
11	492	68.3	137	2	B32522	Ig heavy chain pro
12	488.5	67.8	140	2	PH1482	Ig heavy chain V r
13	488	67.8	137	1	G2MS43	Ig heavy chain pro
14	488	67.8	137	2	F29380	Ig heavy chain pro
15	487.5	67.7	138	1	HVMS17	Ig heavy chain pro
16	487	67.6	136	2	S41600	Ig heavy chain V r
17	486	67.5	469	2	S47483	Ig gamma 2a chain
18	484.5	67.2	140	1	HVMSG7	Ig heavy chain pro
19	484.5	67.2	140	2	PH1484	Ig heavy chain V r
20	482.5	67.0	136	2	PL0208	Ig heavy chain pro
21	480	66.7	137	2	F29380	Ig heavy chain pro
22	477.5	66.3	131	2	A27472	Ig heavy chain pro
23	475	66.0	121	2	S23622	Ig heavy chain V r
24	474.5	65.9	138	2	S21810	Ig heavy chain V r
25	472.5	65.6	140	2	T01407	Ig heavy chain (my
26	471.5	65.5	136	2	B47159	Ig heavy chain V r
27	470.5	65.3	140	2	S04525	Ig heavy chain pro
28	470.5	65.3	142	2	S19245	Ig heavy chain pro
29	470	65.3	117	1	HVMS02	Ig heavy chain pro
30	468.5	65.1	140	2	PH1489	Ig heavy chain V r
31	468	65.0	132	2	S43799	Ig heavy chain V r
32	467.5	64.9	148	2	S29257	Ig heavy chain V r
33	467	64.9	135	2	PS0053	Ig heavy chain pro
34	467	64.9	141	2	A39276	Ig heavy chain pro
35	467	64.9	150	2	PN0444	Ig heavy chain V r
36	467	64.9	474	2	G2MS11	Ig gamma 2b chain
37	466	64.7	118	2	S30265	Ig heavy chain V r
38	465.5	64.7	135	2	PH1493	Ig heavy chain V r
39	464.5	64.4	134	2	S21916	Ig heavy chain V r
40	464.5	64.4	151	2	PL0011	Ig heavy chain pro
41	463	64.3	117	1	HVMS83	Ig heavy chain pro
42	463	64.3	131	2	S21924	Ig heavy chain V r
43	462	64.2	139	2	PS0024	Ig heavy chain pro
44	461.5	64.1	140	2	PH1498	Ig heavy chain V r
45	461	64.0	117	2	S19553	Ig heavy chain V r

ALIGNMENTS

RESULT 1
PL0105
anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C;Accession: PL0105
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma s
A;Reference number: PL0106; MUID:89235583; PMID:2541221
A;Accession: PL0105
A;Molecule type: mRNA
A;Residues: 1-160 <SIL>
A;Note: the authors translated the codon GAC for residues 108 and 109 as Glu
C;Comment: The antibody is one of the cold agglutinins that preferentially bind red b
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: autoantibody; hemagglutinin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-117/Domain: immunoglobulin homology <IMM>
F;49-54/Region: complementarity-determining 1
F;69-84/Region: complementarity-determining 2
F;118-131/Domain: J region <JOI>
F;132-144/Domain: D segment <DSG>
F;145-160/Domain: C region <CRG>

Query Match 71.5%; Score 514.5; DB 2; Length 160;
Best Local Similarity 69.4%; Pred. No. 7.8e-48;
Matches 100; Conservative 9; Mismatches 26; Indels 9; Gaps 2;

Qy 1 MGWRCIIFFLVTATAVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAISWVRQAP 60
Db 1 MKWVTFISLLFLFSSAYSRGVFRRDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCP 60

Qy 61 FQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARAAW 120
Db 61 FEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQE 120

Qy 121 YMDVWGQGTLVTVSS 135
Db 121 PERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELL 180

RESULT 2
HVMSB1
Ig heavy chain precursor V region (BCL1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-200
C;Accession: A03042
R;Knapp, M.R.; Sire, M.F.; Seyfert, N.; Ward, R.H.; Decker, P.W.; Strober, S.; Brattner
Proc. Natl. Acad. Sci. U.S.A. 79, 2996-3000, 1982
A;Title: Simultaneous expression of immunoglobulin mu and delta heavy chains by a <S
A;Reference number: A03042; MUID:82222642; PMID:6806821

A;Accession: A02042
A;Molecule type: mRNA
A;Residues: 1-136 <KNA>
A;Cross-references: GB:J00494; NID:g195010; PIDN:AAA98139.1; PID:g195011
A;Note: the sequence was determined from the differentiated gene
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (BCL1) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 513.5; DB 1; Length 136;
Best Local Similarity 72.1%; Pred. No. 8.1e-88;
Matches 98; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAIQWVRQAP 60
Db 1 MGWSCIIFFLVATATGVHSQVQLQQSGFEVVRPGVSVKISCKGSGYIFIDYAMHWVKQSH 60

Qy 61 GQGLEWIGVINIYYGNINYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAA 119
Db 61 AKSLEWIGVISIYNGNINYNQKFKGKATMTVDKSSSTVYMELARLTSESAIFYCARYYG 120

Qy 120 WYMDYWGQGTLVTVSS 135
Db 121 NYFDYWGQGTILTVSS 136

RESULT 3
E42513
Ig heavy chain precursor V region (MRL22) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
C;Accession: E42513
R;Kotler, R.; Strobal, R.; Balderas, R.S.; Hussain, M.E.; Nusbaum, D.J.; Dechosal, M.A.; J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A44689; MUID:88331394; PMID:3138286
A;Accession: E42513
A;Molecule type: DNA
A;Residues: 1-138 <KOE>
A;Cross-references: GB:M20845; NID:g190945; PIDN:AAA40847.1; PID:g190946
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.2%; Score 512.5; DB 2; Length 138;
Best Local Similarity 72.1%; Pred. No. 1e-87;
Matches 101; Conservative 14; Mismatches 19; Indels 7; Gaps 8;

Qy 1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAIQWVRQAP 60
Db 1 MGWSCIILFLVAAATGVHSQVQLQQSPGAELVEPGASVELSCKASGYTFTSYWINWVEQRP 60

Qy 61 GQGLEWIGVINIY YDNINYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAA 118
Db 61 GQGLEWIG NIYPGSGSINYNEKFKYKATLTVDTSSSTAYMQLSSLTSEDSAVYYCARE 118

Qy 119 WYMDYWGQGTLVTVSS 135
Db 119 YYGNYWGQGTSVTVSS 134

RESULT 4
S49560
anti-Sm autoantibody Vh chain (VH1/DK1 or 9ML2/HH4b) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49560
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Submitted to the EMBL data library, October 1994

A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48747
A;Accession: S49560
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <MAH>
A;Cross-references: EMBL:Z46438; NID:g560849; PIDN:CAA86467.1; PID:g560849
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.1%; Score 512; DB 2; Length 135;
Best Local Similarity 74.8%; Pred. No. 1.1e-87;
Matches 101; Conservative 7; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAIQWVRQAP 60
Db 1 MGWSWIILFLVAAATGAHSQVQLVQSGAEVKKPGASVKVSCKASGYIFIGYYMHWVRQAP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
Db 61 GQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARART 120

Qy 121 YMDYWGQGTLVTVSS 135
Db 121 GYNYWGQGTLVTVSS 135

RESULT 5
A30577
Ig heavy chain precursor V region (MRL10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
C;Accession: A30577
R;Kotler, R., Newman, D.J., Levy, D.E., Wilson, M.C., Moller, N.P.H., Dixon, F.J.; Th
J. Exp. Med. 161, 805-815, 1985
A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r
A;Reference number: A30577; MUID:85159423; PMID:3920443
A;Accession: A30577
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <KOE>
A;Cross-references: GB:M37621
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 510; DB 2; Length 135;
Best Local Similarity 72.4%; Pred. No. 1.6e-87;
Matches 99; Conservative 14; Mismatches 21; Indels 4; Gaps 2;

Qy 1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAIQWVRQAP 60
Db 1 MGWSCIILFLVAAATGVHSQVQLQQTPGAELVKPGASVKLSCKASGYTFTSYWINWVEQRP 60

Qy 61 GQGLEWIGVINIY YDNINYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAA 118
Db 61 GQGLEWIG NIYPGSGSINYNEKFKYKATLTVDTSSSTAYMQLSSLTSEDSAVYYCAREA 118

Qy 119 WYMDYWGQGTLVTVSS 135
Db 119 VGGFAYWGQGTLVTVSA 135

RESULT 6
MBMS18
Ig heavy chain precursor V region (B1-8) - mouse
N;Contains: Ig heavy chain precursor V region 186-2
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C;Accession: A90809; B90809; A22769; A02034; A02036
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore
Cell 24, 625-637, 1981
A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies:

A;Reference number: A90809; MUID:81234548; PMID:6788376
A;Accession: A90809
A;Molecule type: DNA
A;Residues: 1-139 <B18>
A;Cross-references: GB:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115
A;Accession: B90809
A;Molecule type: DNA
A;Residues: 1-117 <B62>
A;Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapt
A;Note: the 18c 2 germline gene was cloned from a library of C57BL/6 DNA
R;Dildrop, R.; Bronsteamann, M.; Radbruch, A.; Rajewsky, K.; Boyreuther, K.
EMBO J. 1, 635-640, 1982
A;Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A;Reference number: A90971; MUID:84236026; PMID:7188353
A;Accession: A22769
A;Molecule type: protein
A;Residues: 20-139 <DIL>
A;Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch vari
 of the mu chain
C;Genetics:
A;Introns: 1c/1
C;Superfamily: Immunoglobulin V region; Immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/PROduct: Ig kappa chain V region (B1-8) #status experimental <MAT
F;34-117/Domain: Immunoglobulin homology <IMM>
F;114-124/Region: D segment
F;125-130/Region: J segment (JH2)

  Query Match 69.6%; Score 501; DB 1; Length 139;
  Best Local Similarity 68.3%; Pred. No. 1e-46;
  Matches 95; Conservative 16; Mismatches 24; Indels 4; Gaps 1;

Qy 1 MGWNCIIFFLVITATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIQWVRQAP 60
 ||||:|| || ||||||||||| | ||| ||||||||||||||| | : ||:| |
Db 1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFKGKAIMIVDRSISTAYMELSSLRSEDTAVYYCAR--- 117
 |:|||||| |: | ||:||| |||:|||| :|||||:|||| |||:|||||||
Db 61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120

Qy 118 AAWYMDYWGQGTLVTVSS 135
 : : |||||| :||||
Db 121 YGSSYFDYWGQGTTLTVSS 139

RESULT 7
A27609
Ig heavy chain precursor V region (129) mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A27609
R;Klein, U.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A;Title: 1.2% lymphoma cells express a nonmutated V-H gene before and after H chain swit
A;Reference number: A27609; MUID:88154467; PMID:3126234
A;Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:M26491; NID:g195411; PIDN:AAA37993.1; PID:g55992
C;Genetics:
A;Introns: 1c/1
C;Superfamily: Immunoglobulin V region; Immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region 129 #status predicted <VAR>
F;34-117/Domain: Immunoglobulin homology <IMM>

  Query Match 69.4%; Score 500; DB 2; Length 139;
  Best Local Similarity 68.3%; Pred. No. 1.2e-46;
  Matches 95; Conservative 16; Mismatches 24; Indels 4; Gaps 1;

Qy 1 MGWNCIIFFLVITATGVHSQVQLVQSGAEVEKPGSSVKVSCKASGYIFTDYAIQWVRQAP 60
 ||| | || ||: || ||||||||| | ||| |||:|||:|||||||||||| : ||:|
Db 1 MGWSCIILFLVATATGVHSQVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKP 60

Qy 61 GQGLEWIGYINPYNDGTKYNEKFKGKATLISDKSSSTAYMELSSLTSEDSAVYYCARYSY 120
 |:|||||| || |:|:|| |||||:|||||:|||||:|||||:|||| ||:|||||
Db 61 GKSLEWIGYINPYNDYTKYNEKFKGKATLTSDKSSSTAYMQLNSLTSEDSAVYYCARYSY 120

Qy 121 Y -- MDYWGQGTLVTVSS 135
 | |||||||| |||||
Db 121 YGLYAMDYWGQGTSVTVSS 139

RESULT 8
JL0076
Ig heavy chain precursor V region (anti phenyloxazolone, 18C10) mouse (treatment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: JL0076
R;Kaartinen, M.; Reina Serra, J.; Mackelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross
A;Reference number: JL0076; MUID:89009973; PMID:3211160
A;Accession: JL0076
A;Molecule type: mRNA
A;Residues: 1-141 <KAA>
A;Cross-references: GB:M27798; NID:g196851; PIDN:AAA39441.1; PID:g196852
C;Superfamily: Immunoglobulin V region; Immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-141/Product: Ig heavy chain #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;50-54/Region: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
F;125-130/Region: JH2 segment
F;136-141/Region: C

  Query Match 69.2%; Score 498; DB 2; Length 141;
  Best Local Similarity 69.6%; Pred. No. 1.9e-46;
  Matches 94; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MGWNCIIFFLVITATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIQWVRQAP 60
 ||||:|| || |||||||||||| | ||| |||:||| :|||||||||| | : ||:| |
Db 1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFKGKAIMIVDRSISTAYMELSSLRSEDTAVYYCARAAW 120
 |:|||||| |: | ||:||| |||:|||| :|||||:|||| |||:|||||||
Db 61 GRGLEWIGRIDPNSGGTKYNEKFESKATLIVERESSTAYMQLSSLTSEDSAVYYCARGDL 120

Qy 121 YMDYWGQGTLVTVSS 135
 ||||||| :||||
Db 121 AMDYWGQGTTLTVSS 135

RESULT 9
A32483
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1999
C;Accession: A32483
R;Carrick, J.W.; Lautenberg, L.; Brenner, C.A.; Abrahamsen, M.; Fry, K.E.; Burchiel, K
Biochem. Biophys. Res. Commun. 160, 1251-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells
A;Reference number: A32483; MUID:89275986; PMID:2499427
A;Accession: A32483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-141 <CAR>
A;Cross-references: GB:M29463
C;Superfamily: Immunoglobulin V region; Immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>

  Query Match 68.7%; Score 494.5; DB 2; Length 142;

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  Best Local Similarity   71.5%;  Pred. No. 3.8e-55;
  Matches   99;  Conservative   10;  Mismatches   18;  Indels   11;  Gaps    1;

Qy          10 EVTLAESGPRLQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAPGQGLEWMGV 69
               ||  . . |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 QLAVAESGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGI 60

Qy          70 INIYYGNSNYNQKFQGRVIMTRDTSISTVYMELSSLRSEDTAVYYCARAAWY 121
               ||     :|||| |||||: ||| | |||| |||||||||||||||||||
Db          61 INPSGGSTNYAQKFQGRVIMTRDTSISTVYMELSSLRSEDTAVYYCARGKLATIIFGVLI 120

Qy         122     MDYWGQGTLVTVSS 135
                   ||||||||||||||
Db         121 YDGMDYWGQGTLVTVSS 137


RESULT 10
S14683
Ig mu chain precursor, membrane bound (clone 201) - human
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1991 #sequence_revision 01-Dec-1991 #text_change 23-Jul-1999
C;Accession: S14683; S08047
R;Friedlander, K.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A;Reference number: S14683; MUID:90342450; PMID:2115996
A;Accession: S14683
A;Molecule type: mRNA
A;Residues: 1-627 <FRI>
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34771.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-627/Product: Ig mu chain #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             98.7%;  Score 444.5;  DB 2;  Length 627;
  Best Local Similarity   95.8%;  Pred. No. 1.7e-55;
  Matches  100;  Conservative   10;  Mismatches   25;  Indels   17;  Gaps    2;

Qy           1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
               |  |     ||||  ||||||||||||||||||||||||||||||||||||||||||||
Db           1 MEWIWVFFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAP 60

Qy          61 GQGLEWMGWINIYYGNSNYNQKFQGRVIMTRDTSISTVYMELSSLRSEDTAVYYCARAAWY 120
               |||||||| ||     || |||||| |||||||||||||||||||||||||||||||||||
Db          61 GQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARIGL 120

Qy         121 MDYWGQGTLVTVSS 135
               :: ||||||||||||
Db         121 LGPYSSWFFNGDYYYYGMDVWGQGTIVTVSS 152


RESULT 11
H42518
Ig heavy chain precursor V region (DXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1999 #text_change 21-Jan-2000
C;Accession: H42518
R;Kotlan, P.; Strehal, P.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Buchosal, M.A.;
J. Clin. Invest. 82, 852-864, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A40889; MUID:88331494; PMID:3140289
A;Accession: H42518
A;Molecule type: DNA
A;Residues: 1-137 <KOT>
A;Cross-references: GB:M20831; NID:g190666; PIDN:AAA38848.1; PID:g190650
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             98.4%;  Score 442;  DB 2;  Length 137;
  Best Local Similarity   96.4%;  Pred. No. 6e-55;

  Matches   91;  Conservative   22;  Mismatches   22;  Indels    2;  Gaps    1;

Qy           1 MGWNCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
               |||| |  ||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MGWSWIFLFLLSVTAGVHSEVQLQQSGAELVRPGASVKLSCTASGFNIKDYYIHWVKQRP 60

Qy          61 GQGLEWIGWIDPENGNTVYDPKFQGKATITADTSSNTAYMQLSSLTSEDTAVYYCNAAWY 120
               |||||||| ||  |  |||||||| |||||||||||||||||||||||||||||||||||
Db          61 EQGLEWIGRIDPENGYTVYDPKFQGKASITADTSSNTAYMQLSSLTSEDTAVYYCNAAWY 120

Qy         121 MDYWGQGTLVTVSS 135
               ||||||| :||||
Db         121 GSSPDYWGQGTILIVSS 137


RESULT 12
PH1482
Ig heavy chain V region (clones 46-95[IG] and X7-7G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1482; PH1495
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transcripts that
d for somatic mutation.
A;Reference number: PH1482; MUID:93171820; PMID:8436910
A;Accession: PH1482
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <SIU>
A;Experimental source: hybridoma cell
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             97.8%;  Score 438.5;  DB 2;  Length 140;
  Best Local Similarity   95.7%;  Pred. No. 1.2e-54;
  Matches   92;  Conservative   18;  Mismatches   25;  Indels    5;  Gaps    1;

Qy           1 MGWNCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
               |||| |  ||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MGWSCIILFLVSVTAGVHSEVQLQQSGAELVRPGASVKLSCTASGFNIKDYYIHWVKQRP 60

Qy          61 GQGLEWIGWIDPENGNTVYDPKFQGKATITADTSSNTAYMQLSSLTSEDTAVYYCANAA 118
               |||||||| ||     | ||||||| |||||||||||||||||||||||||||||||||
Db          61 GQGLEAWIGRIDPENGNTKYAPKFQGKVTITADTSSNTAYMQLSSLTSEDTAVYFCARSVY 120

Qy         119 AWYMDYWGQGTLVTVSS 135
               ::| ||||||| :||||
Db         121 YGGSYYFDYWGQGTTLTVSS 140


RESULT 13
G2MS43
Ig heavy chain precursor V region (S43) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C;Accession: A02038
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore
Cell 24, 625-637, 1981
A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies:
A;Reference number: A00809; MUID:81234548; PMID:6788376
A;Accession: A02038
A;Molecule type: mRNA
A;Residues: 1-137 <BOT>
A;Cross-references: GB:J00539; NID:g195118; PIDN:AAA38172.1; PID:g195119
A;Note: the gamma 2a chain mRNA was cloned from a hybridoma making antibodies to the
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-137/Product: Ig heavy chain V region (S43) #status predicted <MAT>
```

```
F;34-117/Domain: immunoglobulin homology ;IMM
F;118-122/Region: D segment
F;123-137/Region: J segment (JH2)

  Query Match             67.8%;  Score 488;  DB 1;  Length 137;
  Best Local Similarity   67.2%;  Pred. No. 1.3e-35;
  Matches   92;  Conservative   15;  Mismatches   29;  Indels    2;  Gaps    1;

Qy          1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIHWVRQAP 60
              ||:::: ||  |||||||||| | |||  |||:|||:|:|||||||| | : || | |
Db          1 MGWSCIMLFLAATATGVHSQVQLQQSGAEFVKPGASVKLSCKASGYTFTSYYLHWVNQRP 60

Qy         61 GQGLEWIGVINIYYDNINYNQKFKGKAIMIVRDTSIAYMELSSLRSEDTAVYYCA  RA 118
              |:|:|||| |:      | || |: |||:|:|| :||||||:|      :|:|||||  |
Db         61 GKGLEWIGRIDPNSGGIIYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARYRL 120

Qy        119 AWYMDYWGQGTLVTVSS 135
              | |||:|:| :||||
Db        121 GEYFDYWGQGTLLIVSS 137


RESULT 14
F29380
Ig heavy chain precursor V region (AG03.3G/57)  mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: F29380
R;Chen, H.I.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13584, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A;Reference number: A92612; MUID:88007582; PMID:3115981
A;Accession: F29380
A;Molecule type: mRNA
A;Residues: 1-147 <CHE>
A;Cross-references: GB:M17165; GB:J03281; NID:g5409; PID:AAA38294.1; PID:g195410
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology  IMM

  Query Match             67.8%;  Score 488;  DB 2;  Length 137;
  Best Local Similarity   69.9%;  Pred. No. 1.3e-35;
  Matches   96;  Conservative   14;  Mismatches   24;  Indels    4;  Gaps    2;

Qy          1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIHWVRQAP 60
              | || || |||||||||||| | ||| |:|:|||:|:|||||| |, | ||: |
Db          1 MGWNYIILFLVAIATGVHSQVQQQPGAELVKPGTSVKLSCKASGYNFTTYWINWVKLRP 60

Qy         61 GQGLEWIGVINIYYDNINYNQKFKGKAIMIVRDTSIAYMELSSLRSEDTAVYYCAD-  117
              |:|:|||| |      :|||:||| |||:||| |:|||||:|||  :|:|||:|||||
Db         61 GQGLEWIGDIYPGSGSTNYNEKFKSKATLTVDTSSSTAYMQLSSLASEDSALYYCARQVG 120

Qy        118 AAWYMDYWGQGTLVTVSS 135
              ::  |:|||||||||:
Db        121 EIWFA YWGQGTLVTVSA 137


RESULT 15
HVMS17
Ig heavy chain precursor V region (IEP' 1017) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 30-May-1997
C;Accession: A02033
R;Gilliam, A.C.; Shen, A.; Richards, J.E.; Blattner, F.R.; Mushinski, J.F.; Tucker, P.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4164-4168, 1984
A;Title: Illegitimate recombination generates a class switch from C-mu to C-delta in an
A;Reference number: A02033; MUID:84248078; PMID:6429663
A;Accession: A02033
A;Molecule type: mRNA
A;Residues: 1-138 <GIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-138/Product: Ig heavy chain V region (IEP' 1017) #status predicted <MAT>
F;21-112/Region: V segment
F;34-117/Domain: immunoglobulin homology <IMM>
F;118-123/Region: D segment
F;121-138/Region: J segment

  Query Match             67.7%;  Score 487.5;  DB 1;  Length 138;
  Best Local Similarity   69.3%;  Pred. No. 1.5e-35;
  Matches   95;  Conservative   16;  Mismatches   24;  Indels    3;  Gaps    1;

Qy          1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKEPGSSVEVSCKASGYIFTDYAIHWVRQAP 60
              |:|: || ||| ||| ||||||| | ||:: |||:|:|:|||||:|:|:| | ||:| |
Db          1 MGWGYIIIFLVAPATDVHSQVQLQQSGPGLVAPSQSVSITCAVSGFSLTNYWVHWVRQPP 60

Qy         61 GQGLEWLGVINIYYDNINYNQKFEGKAIMIVRETSIAYMELSTLRSEDTAVYYCARAAW 120
              |:|:|||| ||     :|||:||| |||:|||||:|||||:|||  :| |:|||||
Db         61 GQGLEWIGEIYPNNNPDYNCNYNEKFENKATLTVDKSSSTAYMQFSSLTSEDFAVYYCARSDG 120

Qy        121 YMD   YWGQGTLVTVSS 135
              |:|   ,|:||:|:|| |:
Db        121 YYIAWFVYWGQGTLVTFSA 138


Search completed: June 14, 2003, 15:08:12
Job time : 15.4523 secs
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GenCore version 5.1.6
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M protein - protein search, using sw model

Run on: June 14, 2003, 15:02:48 ; Search time 14.333 Seconds
(without alignments)
495.506 Million cell updates/sec

Title: US-09-249-011B-6
Perfect score: 720
Sequence: 1 MGWNCIIFFLVTIATGVHS.....ARAAWYMEYWGQGTLVTVSS 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476428 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	513.5	71.3	136	1	HV15_MOUSE	P01759 mus musculu
2	501	69.6	139	1	HV07_MOUSE	P01751 mus musculu
3	488	67.8	137	1	HV11_MOUSE	P01755 mus musculu
4	487.5	67.7	138	1	HV48_MOUSE	P03980 mus musculu
5	484.5	67.2	140	1	HV02_MOUSE	P01746 mus musculu
6	470	65.3	117	1	HV06_MOUSE	P01750 mus musculu
7	468	64.3	117	1	HV05_MOUSE	P01749 mus musculu
8	447	62.1	117	1	HV04_MOUSE	P01748 mus musculu
9	444	61.7	117	1	HV1B_HUMAN	P01743 homo sapien
10	444	61.7	142	1	HV1C_HUMAN	P01744 homo sapien
11	439	61.0	117	1	HV09_MOUSE	P01753 mus musculu
12	439	61.0	117	1	HV1G_HUMAN	P23083 homo sapien
13	435	60.4	117	1	HV49_MOUSE	P06428 mus musculu
14	429	59.6	117	1	HV10_MOUSE	P01754 mus musculu
15	427.5	59.4	117	1	HV13_MOUSE	P01757 mus musculu
16	427.5	59.4	120	1	HV03_MOUSE	P01747 mus musculu
17	426.5	59.2	117	1	HV12_MOUSE	P01756 mus musculu
18	425	59.0	117	1	HV14_MOUSE	P01758 mus musculu
19	411	57.1	117	1	HV52_MOUSE	P06427 mus musculu
20	408	56.7	118	1	HV51_MOUSE	P06430 mus musculu
21	405	56.2	120	1	HV50_MOUSE	P06429 mus musculu
22	379.5	52.7	121	1	HV01_MOUSE	P01745 mus musculu
23	376.5	52.3	117	1	HV1A_HUMAN	P01742 homo sapien
24	374	51.9	114	1	HV00_MOUSE	P01741 mus musculu
25	362.5	50.3	125	1	HV1F_HUMAN	P06329 homo sapien
26	353	49.0	124	1	HV1D_HUMAN	P01760 homo sapien
27	350.5	48.7	121	1	HV2J_HUMAN	P01771 homo sapien
28	340.5	47.3	119	1	HV31_HUMAN	P01770 homo sapien
29	339	47.1	122	1	HV3C_HUMAN	P01768 homo sapien
30	338	46.9	122	1	HV3B_HUMAN	P01769 homo sapien
31	338	46.9	136	1	HV1A_MOUSE	P01757 mus musculus
32	334.5	46.5	142	1	HV01_RAT	P01805 rattus norv
33	334	46.4	124	1	HV1F_HUMAN	P01761 homo sapien
34	327.5	45.5	115	1	HV3D_HUMAN	P01765 homo sapien
35	324	45.0	114	1	HV01_CANFA	P01784 canis familiaris
36	324	45.0	115	1	HV37_MOUSE	P01807 mus musculus
37	321	44.6	120	1	HV1H_HUMAN	P80431 homo sapien
38	319	44.3	119	1	HV38_MOUSE	P01808 mus musculus
39	318.5	44.2	119	1	HV4L_HUMAN	P01775 homo sapien
40	315	43.8	116	1	HV3I_HUMAN	P01781 homo sapien
41	314.5	43.7	117	1	HV42_MOUSE	P01812 mus musculus
42	314	43.6	119	1	HV43_MOUSE	P01813 mus musculus
43	313	43.5	120	1	HV3E_HUMAN	P01782 homo sapien
44	312.5	43.4	144	1	HV44_MOUSE	P01814 mus musculus
45	311	43.2	114	1	HV36_HUMAN	P01763 homo sapien

ALIGNMENTS

RESULT 1
HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222642; PubMed=6806821;
RA Knapp M.R., Tiller T., Newell N., Ward R.B., Tucker P.W., Strober S.;
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC
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DR EMBL; J00401; AAA98133.1;
DR PIR; A02942; HVMSB1.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFB6DB83E35E CRC64;

Query Match 71.3%; Score 513.5; DB 1; Length 136;
Best Local Similarity 72.1%; Pred. No. 1.7e-44;
Matches 98; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MGWNCIIFFLVTIATGVHSEVQLQQSGPELVKPGASVKMSCKASGYTFTAYVMHWVKQKPG 60
MGWNCIIFFLVTIATGVHSEVQLQQSGPELVKPGASVKMSCKASGYTFTAYVMHWVKQKPG
Db 1 MGWNCIIFFLVTIATGVHSEVQLQQSGPELVKPGASVKMSCKASGYTFTAYVMHWVKQKPG 60

Qy 61 QGLEWIGYINPYNDGTKYNEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARGGYYGS 120
QGLEWIGYINPYNDGTKYNEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARGGYYGS
Db 61 QGLEWIGYINPYNDGTKYNEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARGGYYGS 120

Qy 120 WYMDYWGQGTLVTVSS 135
Db 121 WYMDYWGQGTLVTVSS 136

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              | ||||| :|||
Db        121 NYFDYWGQGTTLTVSS 136


RESULT 2
HV07_MOUSE
ID   HV07_MOUSE     STANDARD;      PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region B1-8/186-2 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   --------------------------------------------------------------------------
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A02034; MHMS18.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN         20    139       IG HEAVY CHAIN V REGION B1-8/186-2.
FT   DOMAIN        20    49        FRAMEWORK 1.
FT   DOMAIN        50    54        COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN        55    68        FRAMEWORK 2.
FT   DOMAIN        69    85        COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN        86    117       FRAMEWORK 3.
FT   DOMAIN       118    124       D SEGMENT.
FT   DOMAIN       125    139       JH2 SEGMENT.
FT   DISULFID      41    115       BY SIMILARITY.
FT   NON_TER      139    139
SQ   SEQUENCE   139 AA;  15419 MW;  1B57DD4FD8C9F465 CRC64;

  Query Match             69.6%;  Score 501;  DB 1;  Length 139;
  Best Local Similarity   68.3%;  Pred. No. 3e-43;
  Matches   95;  Conservative   16;  Mismatches   24;  Indels    4;  Gaps    1;

Qy          1 MGWNWIFLFLVTIAIGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:::: ||  ||||||||||| | |||: |||:|||:||||||||||  | : ||:| |
Db          1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy         61 GQGLEWIGVINTYYDNTNYNQKFKGKATMTVDKSISTAYMELSSLRSEDTAVYYCAR    117
              |:||||||| |:       | ||:||| |||:|||| :|||||:|||| |||:||||||||
Db         61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120

Qy        118  AAWYMDYWGQGTLVTVSS 135
                : | :||||||| :||||
Db        121 YGSSYFDYWGQGTTLTVSS 139
```

```
RESULT 3
HV11_MOUSE
ID   HV11_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01755;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region S43 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE GAMMA 2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   --------------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; J00477; AAA38172.1; -.
DR   PIR; A02038; G2MS43.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN         20    137       IG HEAVY CHAIN V REGION S43.
FT   DOMAIN        20    49        FRAMEWORK 1.
FT   DOMAIN        50    54        COMPLEMENTARITY DETERMINING-1.
FT   DOMAIN        55    68        FRAMEWORK 2.
FT   DOMAIN        69    85        COMPLEMENTARITY DETERMINING-2.
FT   DOMAIN        86    117       FRAMEWORK 3.
FT   DOMAIN       118    122       D SEGMENT.
FT   DOMAIN       123    137       JH2 SEGMENT.
FT   DISULFID      41    115       BY SIMILARITY.
FT   NON_TER      137    137
SQ   SEQUENCE   137 AA;  15200 MW;  ADD5881BF44B8EC9 CRC64;

  Query Match             67.8%;  Score 488;  DB 1;  Length 137;
  Best Local Similarity   67.2%;  Pred. No. 5.9e-42;
  Matches   92;  Conservative   15;  Mismatches   28;  Indels    2;  Gaps    1;

Qy          1 MGWNWIFLFLVTIAIGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:||: ||  |||||||||| | |||  |||:|||:||||||||||  | : || | |
Db          1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYLMHWVNQRP 60

Qy         61 GQGLEWIGVINTYYDNTNYNQKFKGKATMTVDKSISTAYMELSSLRSEDTAVYYCA--RA 118
              |:||||||| |:       | ||: |: |||:|:|| :|||||:|||| |||:||||||  |
Db         61 GRGLEWIGRIDPNSGGTIYNEHFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYEL 120

Qy        119 AWYMDYWGQGTLVTVSS 135
                | ||||||| :||||
Db        121 GRYFDYWGQGTTLTVSS 137


RESULT 4
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```
HV48_MOUSE
ID   HV48_MOUSE      STANDARD;      PRT;   138 AA.
AC   P03980;
DT   28-OCT-1986 (Rel. 02, Created)
DT   28-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Ig heavy chain V region TEPC 1017 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Hoshinski J.P.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN      21     49       FRAMEWORK 1.
FT   DOMAIN      50     54       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN      55     68       FRAMEWORK 2.
FT   DOMAIN      69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      86    117       FRAMEWORK 3.
FT   DOMAIN     118    127       COMPLEMENTARITY DETERMINING 3.
FT   DOMAIN     128    138       FRAMEWORK 4.
FT   DISULFID    41    115       BY SIMILARITY.
FT   N-GLYC     138    138
SQ   SEQUENCE   138 AA;  15576 MW;  748157E4C690788E CRC64;

  Query Match             67.7%;  Score 487.5;  DB 1;  Length 138;
  Best Local Similarity   68.8%;  Pred. No. 6.7e-42;
  Matches   95;  Conservative   16;  Mismatches   24;  Indels    3;  Gaps    1;

Qy          1 MGWNCIIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              ||| | || ||| ||| |||||||| | ||| |||:|||::|||||:||||:| | ||:| |
Db          1 MGWSYIILFLVATATDVHSQVQLQQSGAELVRPGASVQLSCKASGHTFVDYNVHWVKQRP 60

Qy         61 GQGLEWIGVINIYYGNTNYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
              |||||||| ||     :|||:||| |||:|||||:|||||:||| | :|||||||:
Db         61 GQGLEWIGEINPNDGRSNYNEKFKNKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARSDC 120

Qy        121 YMDY  YWGQGTLVTVSS 135
              | |   :|:|||||| |:
Db        121 YYPWFVYWGQGTLVTFSA 138


RESULT 5
HV02_MOUSE
ID   HV02_MOUSE      STANDARD;      PRT;   140 AA.
AC   P01736;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Ig heavy chain V region 9807 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
CC   -!- ---------- ---------- ---------- ---------- ----------
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CC   ---------- ---------- ---------- ---------- ----------
DR   EMBL; J00493; AAA38128.1;  -.
DR   PIR; A02032; HVMS07.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    140       IG HEAVY CHAIN V REGION 9807.
FT   NON_TER    140    140
SQ   SEQUENCE   140 AA;  15513 MW;  [illegible] CRC64;

  Query Match             67.2%;  Score 483.5;  DB 1;  Length 140;
  Best Local Similarity   65.7%;  Pred. No. 1.7e-41;
  Matches   92;  Conservative   17;  Mismatches   26;  Indels    5;  Gaps    1;

Qy          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              ||| | ||:|  ||||||||| |||||:| : ||||| |||||||||| | | ||:| |
Db          1 MGWSYIILFLVSVTAGVHSQVQLQQSGAELVRAGASVKLSCKASGYSFTSYCINWVKQRP 60

Qy         61 GQGLEWIGVINIYYGNTNYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
              ||.|:|||| ||     :|||:||| |||:|||||:|||||:||| | :|||||||:
Db         61 GQGIEWIGEINPSNGNTNYNEKFKNKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARSDC 120

Qy        121 Y -   MDYWGQGTLVTVSS 135
              |   :  |||||||| :|||
Db        121 YGGSYGFDYWGQGTPLTVSS 140


RESULT 6
HV06_MOUSE
ID   HV06_MOUSE      STANDARD;      PRT;   117 AA.
AC   P01750;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Ig heavy chain V region 102 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN C57BL/6;
RX   MEDLINE=81234148; PubMed=6789376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: Somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT CODE FOR V REGIONS OF NP-B ANTIBODIES.
DR   PIR; A02042; HVMS02.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
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FT   SIGNAL          1      19
FT   CHAIN           20     117       IG HEAVY CHAIN V REGION 23.
FT   DOMAIN          20     49        FRAMEWORK 1.
FT   DOMAIN          50     54        COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN          55     68        FRAMEWORK 2.
FT   DOMAIN          69     85        COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN          86     117       FRAMEWORK 3.
FT   DISULFID        41     115       BY SIMILARITY.
FT   NON_TER         20     20
SQ   SEQUENCE   117 AA;  12867 MW;  716A7F08C1F7ABC7 CRC64;

  Query Match             65.8%;  Score 479;  DB 1;  Length 117;
  Best Local Similarity   76.7%;  Pred. No. 3.1e-40;
  Matches   89;  Conservative   11;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:|||| ||| ||||||| ||| | ||| :|||||||:|||||||| | : |||| |
Db          1 MGWSYIILFLVATATGVHSEVQLQQSGAELVKPGASVKLSCTASGFNIKDHWMHWVKQRP 60

Qy         61 GQGLEWIGVINTYYGNTNYNQKFKGKAIMTVDKSSSTAYMELSSLRSEDTAVYYCA 116
              |||:|||| :    :|||||||||||:|||||:|||||:|||| |||:|||||
Db         61 GQGLEWIGEIHPSDSDTNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116


RESULT 7
HV05_MOUSE
ID   HV05_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01715;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1989 (Rel. 08, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 23 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788476;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT SHARE ENCODE V REGIONS OF NPB ANTIBODIES.
CC
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CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; X00496; AAA39065.1; -.
DR   PIR; A02931; HVMS23.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR004596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1      19
FT   CHAIN           20     117       IG HEAVY CHAIN V REGION 23.
FT   DOMAIN          20     49        FRAMEWORK 1.
FT   DOMAIN          50     54        COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN          55     68        FRAMEWORK 2.
FT   DOMAIN          69     85        COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN          86     117       FRAMEWORK 3.
FT   DISULFID        41     115       BY SIMILARITY.
FT   NON_TER         20     20
SQ   SEQUENCE   117 AA;  12867 MW;  716A7F08C1F7ABC7 CRC64;

  Query Match             65.8%;  Score 479;  DB 1;  Length 117;
  Best Local Similarity   76.7%;  Pred. No. 3.1e-40;
  Matches   89;  Conservative   11;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:|||| ||| ||||||| ||| | ||| :|||||||:|||||||| | : |||| |
Db          1 MGWSYIILFLVATATGVHSEVQLQQSGAELVKPGASVKLSCTASGFNIKDHWMHWVKQRP 60

Qy         61 GQGLEWIGVINTYYGNTNYNQKFKGKAIMTVDKSSSTAYMELSSLRSEDTAVYYCA 116
              |||:|||| :    :|||||||||||:|||||:|||||:|||| |||:|||||
Db         61 GQGLEWIGEIHPSDSDTNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116


SQ   SEQUENCE   117 AA;  13016 MW;  42C6A01C53675ED0 CRC64;

  Query Match             64.7%;  Score 464;  DB 1;  Length 117;
  Best Local Similarity   75.7%;  Pred. No. 1.6e-39;
  Matches   90;  Conservative   12;  Mismatches   18;  Indels    4;  Gaps    2;

Qy          1 MGWSYIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:|||| ||| |||||||| | ||| :|||||||||||||||| | : |||| |
Db          1 MGWSFIILFLVATATGVHSEVQLQQSGAELVKPGASVKMSCKASGYTFTSYVMHWVKQKP 60

Qy         61 GQGLEWIGYINPYNDGTKYNEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCAR 117
              |||||||| |||  :  |||||||| ||:|||||:|||||:|||| ||||:|||||
Db         61 GQGLEWIGDINPYNDGTKYNEKFKEKATLTSDKSSSTAYMQLSSLTSEDSAVYYCAK 117


RESULT 8
HV04_MOUSE
ID   HV04_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01748;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 23 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788476;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT SHARE ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; A02040; HVMS23.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR004596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1      19
FT   CHAIN           20     117       IG HEAVY CHAIN V REGION 23.
FT   DOMAIN          20     49        FRAMEWORK 1.
FT   DOMAIN          50     54        COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN          55     68        FRAMEWORK 2.
FT   DOMAIN          69     85        COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN          86     117       FRAMEWORK 3.
FT   DISULFID        41     115       BY SIMILARITY.
FT   NON_TER         117    117
SQ   SEQUENCE   117 AA;  12772 MW;  C530FB2C9C06FC9B CRC64;

  Query Match             62.1%;  Score 447;  DB 1;  Length 117;
  Best Local Similarity   71.8%;  Pred. No. 6.2e-38;
  Matches   84;  Conservative   11;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MGWSYIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:|||| ||| | |||||||| | | |: :|||:|||:|||||||||| | : |||| |
Db          1 MGWSWIFLFMAAVAGVQSEVQLLESGPELVKPGASVKISCKASGYSFTGYFMNWVKQSH 60

Qy         61 GQGLEWIGRINPYNGDTFYNQKFKGKATLTVDKSSSTAYMELLSLTSEDSAVYYCAK 117
              |||||||| ||     |||||||| | |||||:|||| :|||| |:|||||||||
Db         61 GKSLEWIGDINPNNGGTSYNQKFKGKASLTVDKSSRTAYMDLRSLTSEDSAVYYCAK 117


RESULT 9
HV1B_HUMAN
ID   HV1B_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01743;
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ID   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region BG8 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83144028; PubMed=6298778;
RA   Reichart G., Rabbi D., Glazer L., Zakut R., Givol D.;
RT   "Evolutionary aspects of immunoglobulin heavy chain variable region
RT   (VH) gene subgroups.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC   -----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00243; AAA52988.1; -.
DR   PIR; A02024; HVHUBG.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003599; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V-I REGION BG8.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12946 MW;  2D3F92FC60C7D1FE7 CRC64;

  Query Match             61.7%;  Score 444;  DB 1;  Length 117;
  Best Local Similarity   72.6%;  Pred. No. 1.2e-37;
  Matches   85;  Conservative   10;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              | |    :| |:  | | ||||||||||||||||||:|||||||||:|||  | : ||||||
Db          1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAP 60

Qy         61 GQGLEWIGVINIYYDNINYNQKFKGNAIMIVKSLSTATMELSSLRSEDTAVYYCAR 117
              ||||||:|:||    :|:| |||:| || | |||| ||||||||||||||||||| 
Db         61 GQGLEWMGIINPSGGSTSYAQKFQGRVIMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117


RESULT 1
HV1C_HUMAN
ID   HV1C_HUMAN      STANDARD;      PRT;   147 AA.
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1989 (Rel. 10, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region ND precursor (Fragments).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86056254; PubMed=6815656;
RA   Kemben J.D., Molnaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA   Bell L.V., Gould H.J.;
RT   "Cloning and sequence determination of the gene for the human
RT   immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN   [2]
RP   SEQUENCE OF 20-147.
RA   Bentsich H.B., Johansson S.G.O., von Bahr Lindstrom H.;
RL   (In) Bach M.K. (eds.);
RL   Immediate hypersensitivity: modern concepts and developments, pp.1-96,
RL   Marcel Dekker, New York (1978).
CC   -!- MISCELLANEOUS: THIS PROTEIN CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN.
DR   PIR; A02024; EIHUND.
DR   HSSP; P01780; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003599; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    147       IG HEAVY CHAIN V-I REGION ND.
FT   MOD_RES     20     20       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID    41    115
FT   CONFLICT    21     21       T -> V (IN REF. 2).
FT   CONFLICT    53     54       IH -> HI (IN REF. 2).
FT   CONFLICT    67     68       VG -> GV (IN REF. 2).
FT   CONFLICT   125    125       MISSING (IN REF. 2).
FT   NON_TER    147    147
SQ   SEQUENCE   147 AA;  15154 MW;  948BF9E72A5366C20 CRC64;

  Query Match             61.7%;  Score 444;  DB 1;  Length 147;
  Best Local Similarity   59.2%;  Pred. No. 1.6e-37;
  Matches   87;  Conservative   17;  Mismatches   31;  Indels   12;  Gaps    1;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              | |    :| |:  | | ||||||||||||||||||:|||||||||:|||  | : ||||||
Db          1 MDWTWRVFCLLVAAATRVHSQLQLVQSGAEVKEPGTSVKVSCKASGYTFTDSYIHWVRQAP 60

Qy         61 GQGLEWIGVINIYYDNINYNQKFKGNAIMIVKSLSTATMELSSLRSEDTAVYYCAR 117
              ||||||:|:||    :|:| |||:| || | |||| ||||||||||||||||||| 
Db         61 GQGLEWMGIINPSGGSTSYAQKFQGRVIMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117


RESULT 11
HV09_MOUSE
ID   HV09_MOUSE      STANDARD;      PRT;   117 AA.
AC   P01758; P11271;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 186.1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81243548; PubMed=6788876;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS ENTRY WAS MEDLINE GENE BEARING IN A SET OF CLOSELY
CC       RELATED GENES THAT CODE FOR V REGIONS OF NPB ANTIBODIES.
DR   PIR; B02034; HVMS61.
DR   HSSP; P01780; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003599; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V REGION 186.1.
FT   DOMAIN      20     49       FRAMEWORK 1.
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FT   DOMAIN          51      54       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN          59      68       FRAMEWORK 2.
FT   DOMAIN          69      85       COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN          86     117       FRAMEWORK 3.
FT   DISULFID        41     115       BY SIMILARITY.
FT   NON TER        117     117
SQ   SEQUENCE   117 AA;  12800 MW;  [illegible] CRC64;

  Query Match             61.0%;  Score 435;  DB 1;  Length 117;
  Best Local Similarity   70.1%;  Pred. No. 9.7e-37;
  Matches   82;  Conservative   14;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 MGWNCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              :|:|||| ||  |||||||||| | |||| ||:|||:|||||||||| | : |||| |
Db          1 MGWSCIMLFLAATATGVHSQVQLQQSGSELVKPGASVKISCKTSGYTFTDYAIHWVKQAP 60

Qy         61 GQGLEWIGVINTYYGNINYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCAR 117
              |:|||||| |:      | |||||| |||:||| |:|:|||| || |||:|||||||
Db         61 GKGLEWVGIIFPNSGGTKYNQKFKGKATLTVDKSTSTAYMQLSSLKSEDTAVYYCAR 117


RESULT 12
HV1G_HUMAN
ID   HV1G_HUMAN      STANDARD;      PRT;   117 AA.
AC   P23083;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-I region V35 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88299408; PubMed=2841108;
RA   Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA   Ohno H., Fukuhara S., Honjo T.;
RT   "Dispersed localization of D segments in the human immunoglobulin
RT   heavy-chain locus.";
RL   EMBO J. 7:1047-1051(1988).
CC
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CC
DR   EMBL; X07113; CAA29906.1; -.
DR   PIR; S09476; HVIH35.
DR   HSSP; P01775; 2FB4.
DR   InterPro; IPR000596; Ig_MHC.
DR   InterPro; IPR000596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1      19
FT   CHAIN          20     117       IG HEAVY CHAIN V-I REGION V35.
FT   NON TER        117     117
SQ   SEQUENCE   117 AA;  13000 MW;  BE6D7ED64F0CE97BD c8c764;

  Query Match             61.0%;  Score 435;  DB 1;  Length 117;
  Best Local Similarity   73.5%;  Pred. No. 8.2e-37;
  Matches   86;  Conservative    6;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MGWNCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |:|||| ||  |||||||||| | |||| ||:|||:|||||||||| | : |||| |
Db          1 MDWTWRILFLVAAATGAHSQVQLVQSGAEVEKPGASVEVSCKASGYTFIGYYMHWVRQAP 60

Qy         61 GQGLEWIGVINTYYGNINYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCAR 117
              |:|||||| ||      | |||||| |||:||| |:|:|||| || |||:|||||||
Db         61 GQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117


RESULT 13
HV49_MOUSE
ID   HV49_MOUSE      STANDARD;      PRT;   117 AA.
AC   P06328;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region VH558.B4 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578421;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
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CC   or send an email to license@isb-sib.ch).
CC
DR   EMBL; M13708; AAA38606.1; -.
DR   PIR; A02045; MBMSB4.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR000596; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1      19
FT   CHAIN          20     117       IG HEAVY CHAIN V REGION VH558.B4.
FT   DOMAIN         20      49       FRAMEWORK-1.
FT   DOMAIN         50      54       COMPLEMENTARITY DETERMINING-1.
FT   DOMAIN         55      68       FRAMEWORK-2.
FT   DOMAIN         69      85       COMPLEMENTARITY DETERMINING-2.
FT   DOMAIN         86     117       FRAMEWORK-3.
FT   DISULFID       41     115       BY SIMILARITY.
FT   NON TER       117     117
SQ   SEQUENCE   117 AA;  12834 MW;  68862FAC67ABD345 CRC64;

  Query Match             60.4%;  Score 430;  DB 1;  Length 117;
  Best Local Similarity   69.2%;  Pred. No. 9.7e-37;
  Matches   81;  Conservative   14;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MGWNCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |:|||| ||  |||||||||| | |||| ||:|||:|||||||||| | : |||| |
Db          1 MGWSCIMLFLAATATPVHSPVQLQQSGAELVKPGASVKISCKTSGYWMHWVKQRP 60

Qy         61 GQGLEWIGVINTYYGNINYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCAR 117
              |:|||||| ||      | |||||| |||:||| |:|:|||| || |||:|||||||
Db         61 GRGLEWIGNIFPNSGSTKYNQKFKSKATLTVDKSTSTAYMQLSSPTSEDSAVYYCER 117


RESULT 14
HV10_MOUSE
ID   HV10_MOUSE      STANDARD;      PRT;   117 AA.
AC   P01754; P11270;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 145 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81243548; PubMed=6788476;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC   -----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; J00543; AAA38003.1.
DR   PIR; C92034; HVMS45.
DR   HSSP; P01815; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN         2    117       IG HEAVY CHAIN V REGION 145.
FT   DOMAIN        2     49       FRAMEWORK-1.
FT   DOMAIN        50    54       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN        55    68       FRAMEWORK-2.
FT   DOMAIN        69    85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        86   117       FRAMEWORK-3.
FT   NON_TER     117   117
SQ   SEQUENCE   117 AA;  12921 MW;  D37DEBA3F543E096 CRC64;

  Query Match             59.6%;  Score 429;  DB 1;  Length 117;
  Best Local Similarity   69.2%;  Pred. No. 3.9e-36;
  Matches   81;  Conservative   14;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MGWNCIIFFLVATATGVHSQVQLQQSGAELVKPGASVKLSCKASGYTFTDYAIQWVRQAP 60
              ||.||| || ||||| |||| | ||| |||||||| |:|||||| | : ||:| |
Db          1 MGWSCIMLFLAATATGVHSEVQLQQPGAELVKPGASVKLSSKASGYTFTSYWMHWVKQRP 60

Qy         61 GQGLEWIGVINPYYGTSNYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAVYYCARP 117
              |||||||| |:    | ||||| |||||||| ||||||:|:|| ||||||||||
Db         61 GRGLEWIGRIDPSDSYTNYNQKFKDKATLTVDKSSNTAYMQLSSPTSEDSAVYYCAR 117


RESULT 15
HV13_MOUSE
ID   HV13_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01753;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region J558.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80078170; PubMed=6765988;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC       BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1 TO 5 DIFFERENCES, MANY OF
CC       WHICH OCCUR IN THE 3 AND J SEGMENTS.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR   PIR; A26242; MHMSJ5.
DR   HSSP; P01769; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13024 MW;  292E2AF4BE447E41 CRC64;

  Query Match             59.4%;  Score 427.5;  DB 1;  Length 117;
  Best Local Similarity   70.1%;  Pred. No. 5.5e-46;
  Matches   82;  Conservative   15;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          2 QVQLQQSGPELVKPGASVKMSCKASGYTFTDYAIQWVKQRPGQGLEWIGVINPYNGNTNY 79
              :||| ||| :: |||:|||:|||||||||||| :|||:|: |: |||| ||     |:|
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGISY 60

Qy         80 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARWDWYFDVWGAGTTVTVSS 135
              |||||||||:|||||:|||||:|:|| |||:|||||||   || | || || -|||| |
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYFCARSGYWYFDVWGAGTIVIVSS 117


Search completed: June 14, 2003, 15:08:46
Job time : 14.1574 secs
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OM protein - protein search, using sw model

Run on: June 14, 2003, 15:02:49 ; Search time 51.57 Seconds
(without alignments)
549.359 Million cell updates/sec

Title: US-09-249-011B-6
Perfect score: 720
Sequence: 1 MGWNCIIFFLVITAIGVHSQ.....ARAAWYMDYWGQGTLVIVSS 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	498	69.2	278	11	Q921K1	Q921K1 mus musculu
2	484.5	67.3	473	11	Q9D8L4	Q9d8l4 mus musculu
3	474	65.8	488	11	Q91WR1	Q91wr1 mus musculu
4	473	65.7	613	11	Q8VCX7	Q8vcx7 mus musculu
5	466.5	64.7	481	11	Q91WT1	Q91wt1 mus musculu
6	465	64.6	159	4	Q96QS0	Q96qs0 homo sapien
7	464.5	64.4	481	11	Q91WT1	Q91wt1 mus musculu
8	463.5	64.3	614	4	Q96GA6	Q96ga6 homo sapien
9	460	63.9	163	11	Q96PC1	Q96pc1 mus musculu
10	459	63.7	473	11	Q99L25	Q99l25 mus musculu
11	455	63.2	509	4	Q9BRV0	Q9brv0 homo sapien
12	454	63.1	124	4	Q9UL92	Q9ul92 homo sapien
13	454.5	63.1	168	11	Q8VDC9	Q8vdc9 mus musculu
14	451	62.6	481	11	Q8VCV5	Q8vcv5 mus musculu
15	445.5	61.9	142	11	Q924Q1	Q924q1 mus musculu
16	441.5	61.3	119	4	Q9UL94	Q9ul94 homo sapien
17	439.5	61.0	119	4	Q96TY2	Q96ty2 schistosoma
18	439.5	61.0	489	11	Q8VCX4	Q8vcx4 mus musculu
19	437	60.7	116	4	Q9UL89	Q9ul89 homo sapien
20	436.5	60.6	117	11	Q96XE9	Q96xe9 mus musculu
21	434.5	60.3	120	11	Q925S2	Q925s2 mus musculu
22	434	60.3	143	11	Q91V67	Q91v67 mus musculu
23	432.5	60.1	150	4	Q9Y298	Q9y298 homo sapien
24	429.5	59.7	117	11	Q96XF0	Q96xf0 mus musculu
25	426	59.2	143	11	Q924P9	Q924p9 mus musculu
26	423.5	58.8	120	11	Q92008	Q92008 mus musculu
27	423	58.8	109	11	Q9UL75	Q9ul75 mus musculu
28	422.5	58.7	125	4	Q9UL95	Q9ul95 homo sapien
29	421.5	58.5	140	11	Q924P8	Q924p8 mus musculu
30	421.5	58.5	146	11	Q924R8	Q924r8 mus musculu
31	421.5	58.5	497	4	Q8WWY4	Q8wwy4 homo sapien
32	421	58.5	145	11	Q924Q5	Q924q5 mus musculu
33	420	58.3	143	11	Q924Q0	Q924q0 mus musculu
34	420	58.3	145	11	Q924R1	Q924r1 mus musculu
35	420	58.3	145	11	Q924Q9	Q924q9 mus musculu
36	420	58.3	145	11	Q924P7	Q924p7 mus musculu
37	419.5	58.3	146	11	Q924Q3	Q924q3 mus musculu
38	419	58.2	145	11	Q924R4	Q924r4 mus musculu
39	419	58.2	145	11	Q924R3	Q924r3 mus musculu
40	418	58.1	143	11	Q924R0	Q924r0 mus musculu
41	418	58.1	145	11	Q924Q7	Q924q7 mus musculu
42	417.5	58.0	142	11	Q924Q2	Q924q2 mus musculu
43	415.5	57.7	157	4	Q95978	Q95978 homo sapien
44	411	57.1	147	11	Q924R6	Q924r6 mus musculu
45	413.5	57.4	144	11	Q924P5	Q924p5 mus musculu

ALIGNMENTS

RESULT 1
Q921K1
ID Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:18977).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
SQ SEQUENCE 278 AA; 29778 MW; F894F955D0C0948A CRC64;

Query Match 69.2%; Score 498; DB 11; Length 278.
Best Local Similarity 63.8%; Pred. No. 4.2e-42;
Matches 97; Conservative 10; Mismatches 28; Indels 4; Gaps 1;

Qy 1 MGWNCIIFFLVITAIGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYVAIQWVRQAP 60
|||||||| ||| |||||||||||| | ||| ||||||||||||||||||| | | ||||
Db 1 MGWNCIILFLVATATGVHSEVQLVQSGPELVKPGASVKISCKASGYTFTSYVMHWVKQKP 60

Qy 61 GQGLEWIGYINPYNDGTKYNEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARAAWY 120
|||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GYGLEWIGYINPFNDGNKYNEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARAAWY 120

Qy 121 YMDYWGQGTLVIVSS 135
||||||||||||||| |
Db 121 YMDVWGAGTTVTVSS 135

RESULT 2

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Q96MK4
ID   Q96MK4      PRELIMINARY;      PRT:   473 AA.
AC   Q96MK4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 53.6 kDa protein.
GN   ORF1 OR Hypothetical 53.6 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=PANCREAS;
RX   MEDLINE=21065660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tamura M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kikuchi H., Kitsuregawa M.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.",
RL   Nature 409:685-690(2001).
DR   EMBL; AK002696; BAB22414.1;
DR   HSSP; P00561; 7FAB.
DR   MGD; MGI:2144917; Ifh1.
DR   InterPro; IPR000477; RT.
DR   InterPro; IPR003594; HATPase_c.
DR   InterPro; IPR003661; HisK_like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_V.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 3.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS50296; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA;  51909 MW;  9DED7FA5114758BB CRC64;

  Query Match             67.8%;  Score 481.5;  DB 11;  Length 473;
  Best Local Similarity   66.7%;  Pred. No. 1.4e-40;
  Matches   92;  Conservative   18;  Mismatches   25;  Indels    8;  Gaps    1;

Qy          2 MGWNCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYYAIQWVRQAP 61
              | |:: : ||:   ||| |||| |||:| ||||:|:|||:|||||||:| | |:|| |
Db          1 MEWSWVFLFFLSVTAGVHSEVQLQQSGAEVVKPGASVKISCKATGYTFTEYYMNWVKQRP 60

Qy         62 GQGLEWIGVINPYYGNTNYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
              |:|||:|:    :| |||||||||:| ||||||:|:|||| |:|:||||||| :
Db         61 GQGLEWIGEIDPSDSYTNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGDY 120

Qy        121 YMD   YWGQGTSLTVTVSS 135
                    |||||||||||
Db        121 YYGSYFDYWGQGTTLTVTVSA 143


RESULT 3
Q9JWK1
ID   Q9JWK1      PRELIMINARY;      PRT:   466 AA.
AC   Q9JWK1;
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DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 54.0 kDa protein.
GN   A1893585.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018539; AAH18539.1;  .
DR   MGD; MGI:2144917; A1893585.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   488 AA;  52964 MW;  F12068460B400B9D CRC64;

  Query Match             65.8%;  Score 474;  DB 11;  Length 488;
  Best Local Similarity   62.2%;  Pred. No. 4.6e-39;
  Matches   89;  Conservative   21;  Mismatches   25;  Indels    8;  Gaps    1;

Qy          1 MEAGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAP 60
              |:|:| |:|:  |:|:|||||||||||||||||||||||||||| |||:|:|||||||
Db          1 MKSGWSCVFLFLLSVTAGVHSDIQMTQSPSSLSASLGERVTLTCRASQEISGYLSWLQQKP 60

Qy         61 GKGLEWVSVINSYYPNIHYNDKFEGRFAISRDNSKNTLYLQMNSLRAEDTAVYYCARSAAW 120
              |:|||| || |    |:|||||||||||:|:|||||||||||||||||||:|:|||:|:|
Db         61 DQSPQLLIYGASSLESGVPSRFSGSGSGTQYSLKISRMQTEDEGVYFCVQGSHFPWTFGGG 120

Qy        121 YMD   YWGQGTSLTVTVSS 135
                    |||||||||||||
Db        121 YYGSYFDYWGQGTTLTVTVSA 143


RESULT 4
Q8VCX7
ID   Q8VCX7      PRELIMINARY;      PRT:   613 AA.
AC   Q8VCX7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 67.9 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SALIVARY GLAND;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018315; AAH18315.1;  .
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003599; Ig_2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50296; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;  67855 MW;  41A9384D1A4C2B62 CRC64;

  Query Match             65.7%;  Score 474;  DB 11;  Length 613;
  Best Local Similarity   65.0%;  Pred. No. 7.7e-39;
  Matches   89;  Conservative   16;  Mismatches   32;  Indels    2;  Gaps    1;
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Qy          1 MGWNCIIFFLVITATGVHSQVQLVQSGAEVKKPGSSVKVSCKAS GYTFTSYAIGWVRQAP 60
              ||  :  |:::  ||||||||| ||||| |||:|||:||||:|||| | ||||| |
Db          1 MEWIWVFFLFLLSVTAGVNSQVQLQQSGPELVKPGASVKISCKAS GYSFTGYWMNWVKQRP 60

Qy         61 GQGLEWIGMIDPSDSETHYNQKFKDKATLTVDKSSSTAYMELSSLRSEDTAVYYCAR    117
              |||||||| |: :   |:|||||||  |:||| |:|:||| ||:| |||:|||:|||
Db         61 GQGFEWIGAIDPFDSYTSYNQKFKGKATLTVDTSSSTAYMELSSLTSEDSAVYFCARSD 120

Qy        118 AAWYMDYWGQGTLVTVSS 135
              :: :  |||||| ||||
Db        121 DSSGY--YWGQGTLVTVSS 136


RESULT 6
Q96QS0
ID   Q96QS0      PRELIMINARY;      PRT;   159 AA.
AC   Q96QS0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative matrix cell adhesion molecule 3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilson M.D.;
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RT   "Human sapiens; Putative matrix cell adhesion molecule 3, Ig like domain 3
RL   mRNA (Matrix Cell Adhesion Molecule 3, Mad CAM 3).";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY039025; AAK82649.1; -.
DR   InterPro; IPR003599; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   159 AA;  17922 MW;  7CB1A1E0A1A0E0A0 CRC64;

  Query Match             64.6%;  Score 465;  DB 4;  Length 159;
  Best Local Similarity   61.7%;  Pred. No. 9.6e-59;
  Matches   92;  Conservative   15;  Mismatches   28;  Indels   14;  Gaps    1;

Qy          1 MGWNCIIFFLVITATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAIGWVRQAP 60
              ||  :| |:    | ||||| ||||||||||||||||||||||||||:: : ||||||
Db          1 MEWIGWVFLLAVLQGVQSEVQLVQQSAEVKKPGASVKVSCKASGYTFTSNYYMNWVRQAP 60

Qy         61 GQGLEWIGVINPSTGSTNYNEKFKTRATMTVDKSTSTAYMELSSLRSEDTAVYYCARAA  120
              || ||||||     :  |||||:: ||   || | | | ||||||||| ||||||
Db         61 GQGFEWMGVINPSSGSARYSQKFQGRLIMTRDTSTSTVYMELSSLRSEDTAVYYCARSME 120

Qy        120         WYMDYWGQGTLVTVSS 135
                      : || |||||  |||
Db        121 TTPSGAVSKGFYYYGMDVWGQGTLVTVSS 149


RESULT 7
Q91WII
ID   Q91WII      PRELIMINARY;      PRT;   493 AA.
AC   Q91WII;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical 52.1 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011490; AAH11490.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 4.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   481 AA;  52105 MW;  97DF08D159463F65 CRC64;

  Query Match             64.4%;  Score 463.5;  DB 11;  Length 481;
  Best Local Similarity   65.4%;  Pred. No. 5.1e-48;
  Matches   99;  Conservative   13;  Mismatches   33;  Indels    1;  Gaps    1;

Qy          1 MGWNCIIFFLVITATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAIGWVRQAP 60
              ||  |  ||::   ||  |||||||| |: |||||||||||||||||||| | |||| |
Db          1 MEWRWIFFLFLLSGTAGVLSQVQLQESGPGLVKPSASVKISCKASGYIFISYYIHWVKQRP 60

Qy         61 GQGLEWIGVINPYYGSTNYNEKFKTRATMTVDKSTSTAYMELSSLRSEDTAVYYCARAA 118
              |||| || |     :|  |||||||| ||| |||||||||||||||||||| | | |||| |
Db         61 GQGLVWIGAIYPGNSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARVHDIF 120

Qy        120 WYMDYWGQGTLVTVSS 135
              |  |||||||  :|||
Db        121 WAFDYWGQGALVTVSS 136


RESULT 8
Q96GA6
ID   Q96GA6      PRELIMINARY;      PRT;   514 AA.
AC   Q96GA6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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DE   Unknown (protein for MGC:15420).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC000434; AAH00434.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000539; Ig_C2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   614 AA;  67921 MW;  5EEF549E77AA9BBB CRC64;

  Query Match             64.0%;  Score 460.5;  DB 1;  Length 614;
  Best Local Similarity   66.4%;  Pred. No. 1.4e-47;
  Matches  361;  Conservative  141;  Mismatches  28;  Indels  5;  Gaps  2;

Qy          1 MGWNTIIFFLVFIATGVHSEVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPG 60
              |  |  | |||  ||  ||||||||||||||| ||||||||||||||||| |||||||
Db          1 MSWIWLFLFLVAAATGAHSQMQLVQSGAEVKKPGESLRISCKGSGYIFTSYWIHWVRQMPG 60

Qy         61 KGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR     117
              |  | |||  |  : |||| ||| : |||| ||| ||||||||||||||||||||||||
Db         61 KGLEWMGWIYPENSDTEYNPAFRGQVTISADKSISTAYLQWSSLKASDTAMYYCAR     120

Qy        118 AAW--YMDYWGQGTLVTVSSS 135
              ||:  :  :  |||||||||
Db        121 SSWGQAFDIWGQGTMVTVSSS 140


RESULT 9
Q99L34
ID   Q99L34      PRELIMINARY;      PRT:   363 AA.
AC   Q99L34;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
GN   IGH-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC000434; AAH00434.1; -.
DR   HSSP; P01842; 7FAB.
DR   MGD; MGI:96113; Ighv4-1.
DR   InterPro; IPR000539; Ig.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003599; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00406; IG; 2.
DR   SMART; SM00407; IGC1; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
SQ   SEQUENCE   363 AA;  41007 MW;  EAA6ZA9C9BBE3D2B4 CRC64;

  Query Match             64.0%;  Score 460.5;  DB 11;  Length 363;
  Best Local Similarity   62.6%;  Pred. No. 1.1e-47;
  Matches  361;  Conservative  141;  Mismatches  28;  Indels  5;  Gaps  2;

Qy          1 MGWNTIIFFLVFIATGVHSEVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPG 60
              |  |  | |||  ||  ||||||||||||||| ||||||||||||||||| |||||||
Db          1 MSWIWLFLFLVAAATGAHSQMQLVQSGAEVKKPGESLRISCKGSGYIFTSYWIHWVRQMPG 60

Qy         61 KGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR     117
              |  | |||  |  : |||| ||| : |||| ||| ||||||||||||||||||||||||
Db         61 KGLEWMGWIYPENSDTEYNPAFRGQVTISADKSISTAYLQWSSLKASDTAMYYCAR     120

Qy        118 AAW--YMDYWGQGTLVTVSSS 135
              ||:  :  :  |||||||||
Db        121 SSWGQAFDIWGQGTMVTVSSS 140


RESULT 10
Q99L25
ID   Q99L25      PRELIMINARY;      PRT:   473 AA.
AC   Q99L25;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to RIKEN cDNA 1810060O09 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC000434; AAH00434.1; -.
DR   HSSP; P01842; 7FAB.
DR   InterPro; IPR000539; Ig.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGC1; 1.
DR   SMART; SM00406; IGV; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA;  52449 MW;  BE9889B7986DA155 CRC64;

  Query Match             63.7%;  Score 459;  DB 11;  Length 473;
  Best Local Similarity   60.1%;  Pred. No. 1.4e-47;
  Matches  361;  Conservative  126;  Mismatches  109;  Indels  8;  Gaps  1;

Qy          1 MGWNTIIFFLVFIATGVHSEVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPG 60
              |  |  | |||  ||  ||||||||||||||| ||||||||||||||||| |||||||
Db          1 MSWIWLFLFLVAAATGAHSQMQLVQSGAEVKKPGESLRISCKGSGYIFTSYWIHWVRQMPG 60

Qy         61 KGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR     117
              |||||||  |      :| |:|||||||:| |||:|||||:|:|| |||:|| :|:|
Db         61 KGLEWMGWIYPGYTKGKTEYNEEFEGKATITADEDTSTDTAYMELSSLRSEDTAVYFCSRGGS 120

Qy        118 AAW--YMDYWGQGTLVTVSSS 135
                   :| |||||||:|||||
Db        121 YYYGGYGLYYFDYWGQGTTIVSS 143


RESULT 11
Q9BKV0
ID   Q9BKV0      PRELIMINARY;      PRT:   560 AA.
AC   Q9BKV0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 54.2 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Strausberg R.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC000451; AAH00451.1; -.
DR   HSSP; P17609; 1MCE.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007497; Ig_gel.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGV; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS50200; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   500 AA;  54154 MW;  0A9BF443F2A0C6D4 CRC64;

  Query Match             63.2%;  Score 455;  DB 4;  Length 500;
  Best Local Similarity   61.2%;  Pred. No. 3.8e-37;
  Matches   90;  Conservative   14;  Mismatches   72;  Indels   12;  Gaps    1;

Qy          1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKV  FAASGYTFTSYAIQWVRQAP 60
              | ||   | |||  |||  ||| ||||||||  ||:||:|||| ||:|  |:|  ||||||
Db          1 MDWTWSILFLVAAATGAQSQVHLVQSGAEVMSPGASVKV  CKTSGYTFTSYSIHWVRQAP 60

Qy         61 QGLEWMGWISPSSGNIRFAKKFQQRVTLTTDTSTSTVYMELRSLRSDDTAVYYCARKYC 120
              |||||||| |:   |:|  : ||||: |:| : |||: ||||  |:|:|||||||||
Db         61 QGQGLEWMGWISPSSDNIRFAKKFQQRVTLTTDTSTSTVYMELRSLRSDDTAVYYCARKYC 120

Qy        119         AWYMDYWGQGTLVTVSS 135
                      :|||| |:|:| ||||| 
Db        121 SYSS-SNGYYYYYMDVWGKGTIVTVSS 147


RESULT 12
Q90UL92
ID   Q90UL92       PRELIMINARY;      PRT;   124 AA.
AC   Q90UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22271454; PubMed=11041241;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin reactive autoantibodies in rheumatic carditis and normal
RT   tetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF045022; AAD52658.1; -.
DR   HSSP; P01742; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGV; 1.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;  13796 MW;  DBAAAC8D270AC12A2 CRC64;

  Query Match             63.1%;  Score 454;  DB 4;  Length 124;
  Best Local Similarity   71.0%;  Pred. No. 9.1e-38;
  Matches   88;  Conservative   13;  Mismatches   15;  Indels    8;  Gaps    1;

Qy          1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAIQWVRQAP 60
              | ||   | |||  |||  ||| ||||||||  ||:||:|||| ||:|  |:|  ||||||
Db          1 MDWTWSILFLLSVIAGVHSQVQLQQSGSELMKPGASVKISCKATGYIFSSYWIEWVKQRP 60

Qy         61 QGLEWIGEILPGSGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARSTMI 120
              |||||| |  |||:|:|||| |:|:|:|||||||||||||||||||||||||||||||
Db         61 EGLEWIGEILPGSGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARSTMI 120

Qy        121 TNWYFDVWGAGTTVTVSS 138
              |||||||||| |||||||
Db        121 TNWYFDVWGQGTTVTVSS 138


RESULT 13
Q8VDC9
ID   Q8VDC9       PRELIMINARY;      PRT;   168 AA.
AC   Q8VDC9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Anti-MOG 2/12 variable gamma 2a (Fragment).
GN   IGG2A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Chernajovsky Y.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Sombi P.;
RT   "Targeting t cells to the CNS.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ416332; CAC94867.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   InterPro; IPR001230; Prenyl_site.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
FT   NON_TER     168    168
SQ   SEQUENCE   168 AA;  18293 MW;  1E5719EC70E72723 CRC64;

  Query Match             63.0%;  Score 453.5;  DB 11;  Length 168;
  Best Local Similarity   61.6%;  Pred. No. 1.4e-37;
  Matches   85;  Conservative   16;  Mismatches   34;  Indels    3;  Gaps    1;

Qy          1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAIQWVRQAP 60
              | ||   | |||  |||  ||| ||||||||  ||:||:|||| ||:|  |:|  ||||||
Db          1 MEWIWVFLFLLSVIAGVHSQVQLQQSGSELMKPGASVKISCKATGYIFSSYWIEWVKQRP 60

Qy         61 QGLEWIGEILPGSGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARSTMI 120
              |||||| |  |||:|:|||| |:|:|:|||||||||||||||||||||||||||||||
Db         61 EGLEWIGEILPGSGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCANYGNS 120

Qy        121 TNWYFDVWGAGTTVTVSS 138
              |||||||||| |||||||
Db        121 SRWYFDVWGAGTIVTVSS 138


RESULT 14
Q8VCV5
ID   Q8VCV5       PRELIMINARY;      PRT;   481 AA.
AC   Q8VCV5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
```

```
ID   ol MAR 2002 (TrEMBLrel. 20, Last Sequence update)
DT   ol JUN 2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 72.5 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY TUMOR;
RA   Strausberg R.;
RL   Submitted (DEC 2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010435; AAH10435.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig; 4.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   ProDom; PD000296; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   481 AA;  52326 MW;  52844C58A2607143 CRC64;

  Query Match             62.6%;  Score 451;  DB 11;  Length 481;
  Best Local Similarity   61.6%;  Pred. No. 9e-47;
  Matches   85;  Conservative   25;  Mismatches   24;  Indels    4;  Gaps    2;

Qy          1 MGWNCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIQWVRQAP 60
              | :| :  |:::  ||||||:|| ||| |: :|||||||||||||||:| || | ||:|:
Db          1 MEWSWIFLFLLSGTTGVHSEIQLQQSGPELVRPGISVKVSCKASGYSFTDYNIYWVKQSH 60

Qy         61 GQSLEWIGVINIYYGNTNYNQKFKGKATMTVDKSSSTAYMELSSLRSEDTAVYYCARR-- 117
              |: |||| | |   ::|||||||||||||:|||:|||:|| |::| |||| ||||
Db         61 GKSLEWIGYIYPYNGGTGYNQKFKSKATLTVDKSSNTAYMELNSLTSEDSAVYYCARKWY 120

Qy        118 AAWYMDYWGQGTLVTVSS 135
               ||:  :|||||||||:
Db        121 GAWFA FWGQGTLVTVSA 137


RESULT 15
Q9Z4Q1
ID   Q9Z4Q1       PRELIMINARY;      PRT;   142 AA.
AC   Q9Z4Q1;
DT   01-DEC-2000 (TrEMBLrel. 16, Created)
DT   01-DEC-2000 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   V,2-D-D-J mu protein (Fragment).
GN   V,2-D-D-J MU.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma I.;
RT   "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT   Affinity Maturation of B Cell Antigen Receptors in Response to (4
RT   Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL   Submitted (AUG 2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB062916; BAB69429.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; Ig; 1.
FT   NON_TER       1       1
FT   NON_TER     142     142
SQ   SEQUENCE   142 AA;  15622 MW;  34A26C6E4EA41C8B CRC64;

  Query Match             31.9%;  Score 229.5;  DB 11;  Length 142;
  Best Local Similarity   73.5%;  Pred. No. 7e-17;
  Matches   86;  Conservative   10;  Mismatches   23;  Indels    1;  Gaps    1;

Qy         20 QVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIQWVRQAPGQGLEWIGVINIYYGNTN 79
              |||| | | |: |||:|||:|||||||||| | : |||| |||||||| ||     |||
Db          1 EVQLQQSGPELVRPGISVKVSCKASGYSFTDYNIYWVKQSHGKSLEWIGYIYPYNGGTG 60

Qy         80 NQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARRGWFAMDYWGQGTLVTVSS 135
              :|:|| |||:|||||:|||||:|||| |||:|||||  |  |||||||| ||||
Db         61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARKGWEAMDYWGQGTSVTVSS 117


Search completed: June 14, 2003, 17:12:24
Job time : 53.574 secs
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GenCore version 5.1.6
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SM protein - protein search, using sw model

Run on: June 14, 2003, 15:02:48 ; Search time 49.5506 Seconds
(without alignments)
863.040 Million cell updates/sec

Title: US-09-249-011B-6
Perfect score: 720
Sequence: 1 MGWNCIIFFLVTTATGVHSQ.....ARAAWYMDYWGQGTLVTVSS 135

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 183250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101902:*
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2: /SIDS2/pcdata/geneseq/geneseq-embl/AA1991.DAT:*
3: /SIDS2/pcdata/geneseq/geneseq-embl/AA1987.DAT:*
4: /SIDS2/pcdata/geneseq/geneseq-embl/AA1985.DAT:*
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19: /SIDS2/pcdata/geneseq/geneseq-embl/AA1999.DAT:*
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21: /SIDS2/pcdata/geneseq/geneseq-embl/AA2001.DAT:*
22: /SIDS2/pcdata/geneseq/geneseq-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	720	100.0	135	21	AAB07965	A heavy chain vari
2	427	82.1	135	21	AAB07968	Amino acid sequenc
3	585.5	81.3	470	21	AAW90935	Humanised anti-Fas
4	585.5	81.3	470	23	ABB74904	Mouse humanised an
5	582.5	80.9	470	21	AAW90933	Humanised anti-Fas
6	582.5	80.9	470	23	ABB74902	Humanised anti-Fas
7	581.5	80.8	470	21	AAW90934	Humanised anti-Fas
8	581.5	80.8	470	23	ABB74903	Mouse humanised an
9	579.5	80.5	470	19	AAW83037	Anti-Fas humanised
10	579.5	80.5	470	21	AAB14779	Humanised anti Fas
11	579.5	80.5	470	21	AAW90929	Humanised HFE7A de
12	579.5	80.5	470	23	ABB74898	Humanised anti Fas
13	579.5	80.5	470	23	ABB74944	Humanised anti Fas
14	573.5	79.7	140	15	AAR65550	DREG 200 Humanised
15	567.5	78.8	470	21	AAW90936	Humanised HFE7A de
16	567.5	78.8	470	23	ABB74945	Humanised anti Fas
17	566.5	78.7	145	19	AAW83038	Anti Fas humanised
18	566.5	78.7	145	21	AAB14775	Fragment of humani
19	566.5	78.7	145	21	AAW90925	Humanised anti Fas
20	566.5	78.7	145	23	ABB74894	Humanised anti Fas
21	566.5	78.7	145	23	ABB74940	Humanised anti Fas
22	566.5	78.7	470	19	AAW83036	Anti Fas humanised
23	566.5	78.7	470	21	AAB14776	Humanised anti Fas
24	566.5	78.7	470	21	AAW90926	Humanised HFE7A de
25	566.5	78.7	470	23	ABB74895	Humanised anti Fas
26	566.5	78.7	470	23	ABB74941	Humanised anti Fas
27	554	76.9	588	19	AAW73880	Anti human Fas hum
28	554	76.9	588	21	AAB12917	Anti human Fas hum
29	547	76.0	515	22	AAM52162	Humanised HMFG-1 F
30	547	76.0	517	22	AAM52154	Humanised HMFG-1 F
31	547	76.0	519	22	AAM52164	Humanised HMFG-1 F
32	547	76.0	519	22	AAM52165	Humanised HMFG-1 F
33	547	76.0	521	22	AAM52163	Humanised HMFG-1 F
34	547	76.0	525	22	AAM52166	Humanised HMFG-1 F
35	547	76.0	527	22	AAM52155	Humanised HMFG-1 F
36	547	76.0	529	22	AAM52168	Humanised HMFG-1 F
37	547	76.0	531	22	AAM52167	Humanised HMFG-1 F
38	547	76.0	729	22	AAM52158	Humanised HMFG-1 h
39	547	76.0	730	22	AAM52157	Humanised HMFG-1 h
40	547	76.0	731	22	AAM52156	Humanised HMFG-1 h
41	547	76.0	739	22	AAM52161	Humanised HMFG-1 h
42	547	76.0	740	22	AAM52160	Humanised HMFG-1 h
43	547	76.0	741	22	AAM52159	Humanised HMFG-1 h
44	546	75.8	135	23	AAE24193	Humanised anti Fas
45	547	75.8	135	21	AAB36465	Anti Fas heavy cha

ALIGNMENTS

RESULT 1
AAB07965
ID AAB07965 standard; Protein; 135 AA.
XX
AC AAB07965;
XX
DT [illegible]
XX
DE Anti-Fas variable region : humanised 4S1 antibody.
XX
KW Antibody 4S1; B7 molecule; B7; humanised immunoglobulin;
KW [illegible] disease; inflammatory disorder;
KW systemic lupus erythematosus; diabetes mellitus; encephalitis; asthma;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note "signal peptide"
FT Protein 20..135
FT /note "mature protein"
FT Region 50..54
FT /note "complementarity determining region 1"
FT Region 69..85
FT /note "complementarity determining region 2"
FT Region 118..124
FT /note "complementarity determining region 3"

XX
PN WO200012725-A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US03303.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524542/47.
DR N-PSDB; AAA59692.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infections diseases
XX
PS Example 1; Fig 1A; 162pp; English.
XX
CC The present sequence represents the heavy chain variable region
CC of the humanised murine antibody 3D1. The antibody has a binding
CC specificity to B7 molecules. The antibody is used to construct humanized
CC immunoglobulins, which comprise an antigen binding region of non-human
CC origin and a portion of a human immunoglobulin. The humanized
CC immunoglobulins are useful for treating autoimmune diseases, infections
CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 135 AA;

Query Match 100.0%; Score 720; DB 21; Length 135;
Best Local Similarity 100.0%; Pred. No. 4.3e-55;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGWNCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
Db 1 MGWNCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60

Qy 61 GQGLEWIGVINIYYGNINYNQKFKGRATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
Db 61 GQGLEWIGVINIYYGNINYNQKFKGRATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120

Qy 121 YMDYWGQGTLVTVSS 135
Db 121 YMDYWGQGTLVTVSS 135

RESULT 2
AAB07963
ID AAB07963 standard; Protein; 135 AA.
XX
AC AAB07963;
XX
DT 14-NOV-2000 (first entry)
XX
DE Amino acid sequence of heavy chain variable region 1 3D1 antibody 1.
XX
KW Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW autoimmune disease; infectious disease; inflammatory disorder;
KW systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia, lymphoma, anaemia, sickle cell anaemia, thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note "signal peptide"
FT Protein 20..135
FT /note "mature protein"
FT Region 50..54
FT /note "complementarity determining region 1"
FT Region 69..85
FT /note "complementarity determining region 2"
FT Region 118..124
FT /note "complementarity determining region 3"
XX
PN WO200047625-A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US03303.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524542/47.
DR N-PSDB; AAA59692.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infections diseases -
XX
PS Example 1; Fig 1A; 162pp; English.
XX
CC The present sequence represents the heavy chain variable region of the
CC murine antibody 3D1. The antibody has a binding specificity to B7
CC molecules. The antibody is used to construct humanized immunoglobulins,
CC which comprise an antigen binding region of non human origin and a
CC portion of a human immunoglobulin. The humanized immunoglobulins are
CC useful for treating autoimmune diseases, infectious diseases,
CC inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 135 AA;

Query Match 87.1%; Score 627; DB 21; Length 135;
Best Local Similarity 84.4%; Pred. No. 5.5e-47;
Matches 114; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MGWNCIILFLVATATGVHSQVQLVQSGAEVEKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
Db 1 MGWNCIILFLVATATGVHSQVQLQQSGPELVEPGSSVKISCKASGYTFTDYAIQWVKQSH 60

Qy 61 GQGLEWIGVINIYYGNINYNQKFKGRATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
Db 61 GKSLEWIGVINIYYGNINYNQKFKGKATLTVDKSSSTAYMELASLTSEDSAVYYCASAAW 120

Qy 121 YMDYWGQGTLVTVSS 135
Db 121 YMDYWGQGTLVTVSS 135

```
Db         121 YMDYWGQGTSVTVSS 135


RESULT 3
AAW90435
ID   AAW90435 standard; Protein; 470 AA.
XX
AC   AAW90435;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Humanised anti-Fas designed heavy chain Hou 3 protein.
XX
KW   Fas; antibody; human; anti inflammatory; anti-anemic; antidiabetic;
KW   anti allergic; anti arthritic; antiviral; immunomodulatory; cardiant;
KW   dermatological; immunosuppressive; thyromimetic; antirheumatic; anti Fas;
KW   nephrotropic; antiinfertility; neuroprotective; antiatherosclerotic;
KW   hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW   Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW   Sjorgen's syndrome; anemia, Addison's disease; scleroderma; sterility;
KW   Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW   multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW   insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW   cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS   Synthetic.
XX
PN   EP990663-A2.
XX
PD   05-APR-2000.
XX
PF   29-SEP-1999;   99EP-0307711.
XX
PR   30-SEP-1998;   98JP-0276881
PR   30-SEP-1998;   98JP-0276882.
XX
PA   (SANY ) SANKYO CO LTD.
XX
PI   Serizawa N, Hamayama H, Nakahara K, Tamaki I, Takahashi I;
XX
DR   WPI; 2000-258930/23.
DR   N-PSDB; AAA11646.
XX
PT   New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT   inflammatory or autoimmune disease, induces apoptosis selectively in
PT   cells with abnormal Fas-Fas ligand systems
XX
PS   Claim 2; Page 180-182; 264pp; English.
XX
CC   This invention describes a novel humanized anti-Fas antibody like
CC   molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC   ligand system, by binding to Fas on the cell surface, and prevents
CC   apoptosis in cells with a normal system, by inhibiting binding between
CC   Fas and its ligand. The products of the invention have anti-inflammatory,
CC   anti anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
CC   immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC   antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC   antiatherosclerotic, cardiant and hepatropic activity. (I) induce
CC   apoptosis by binding to cell surface Fas or inhibit it by competitive
CC   inhibition of ligand binding. (I) are used to treat and/or prevent
CC   diseases associated with the Fas/Fas ligand system, especially systemic
CC   lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC   versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC   anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC   disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC   multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC   dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC   cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC   (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC   inhibit apoptosis in normal cells but selectively induce it in abnormal
CC   cells. They bind to both human and murine Fas, so can be evaluated in
CC   murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC   the native ligand, do not induce liver disease, and have reduced risk of
CC   inducing a human anti-murine antibody response. This sequence represents
CC   a humanised anti Fas antibody heavy chain construct designated Hou 3
CC   which is described in the method of the invention.
XX
SQ   Sequence   470 AA;

  Query Match             81.8%;  Score 585.5;  DB 21;  Length 470;
  Best Local Similarity   81.4%;  Pred. No. 8e-43;
  Matches  114;  Conservative    6;  Mismatches   15;  Indels    1;  Gaps    1;

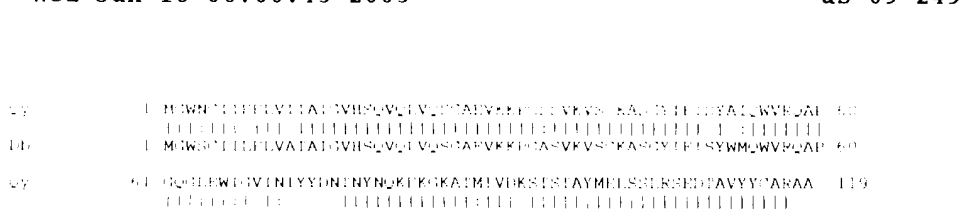
Qy          1 MEAG-LLFLVTLA-VLQGVQCEVQLVQSGAEVKKPGESLKISCKGSGYSFTTYWIGWVRQMPGKG 64
              ||||:|| ||| |||||||||||:|||:|||||:|||||||||||||| | ||||||||
Db          1 MGWS-CIILFLVATATGVHSEVQLVQSGAEVKKPGESLKISCKGSGYSFAIYWIGWVRQMPGKG 60

Qy         65 LEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHD-YYGSGSYY 128
              |||||| |:    :|||||||||||||:||| ||||||||||||||||||||||||
Db         61 LEWMGIIYPGDSDTRYNPSFEGEATISVDTSISTAYLQWSSLKASDTAMYYCARNKDYYGSGSYY 120

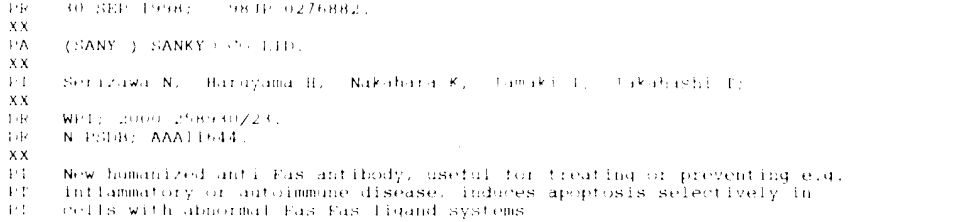
Qy        129      WYFDVWGQGTLVTVSS 145
                   |||:|||||||||||
Db        121 YSNNWYFDVWGQGTLVTVSS 140


RESULT 4
ABR74904
ID   ABR74904 standard; Protein; 470 AA.
XX
AC   ABR74904;
XX
DT   26-APR-2002  (first entry)
XX
DE   Mouse humanised anti Fas antibody related protein SEQ ID NO 9.
XX
KW   Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
KW   light chain subunit; apoptosis; immunosuppressive; antiallergic;
KW   autoimmune disease; allergy; atopic.
XX
OS   Mus musculus.
XX
PN   JP2001342148-A.
XX
PD   11-DEC-2001.
XX
PF   28-MAR-2001; 2001JP-0093106.
XX
PR   29-MAR-2000; 2000JP-0090918.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2002-145114/19.
DR   N-PSDB; ABL45926.
XX
PT   Drug containing humanised anti-Fas antibody, used for preventing and
PT   treating autoimmune diseases, allergy, and atopy
XX
PS   Example 4 (Preparatory); Page 79-80; 194pp; Japanese.
XX
CC   The invention relates to a preventive or treating agent for diseases
CC   related to abnormality in Fas/Fas ligand system containing as the active
CC   component an antibody having as the light chain subunit a polypeptide
CC   containing residues 1-214 of one of 3,239 residue amino acid sequences,
CC   or residues 1-451 of one of 3,470 residue amino acid sequences, all
CC   fully defined in the specification and having an activity of combining
CC   specifically with mammalian Fas and an activity of inducing apoptosis
CC   in a cell expressing Fas. The agent has immunosuppressive and
CC   antiallergic activity and is used for preventing and treating autoimmune
CC   diseases, allergy, atopy and others.
XX
SQ   Sequence   470 AA;

  Query Match             81.8%;  Score 585.5;  DB 23;  Length 470;
  Best Local Similarity   81.4%;  Pred. No. 8e-43;
  Matches  114;  Conservative    6;  Mismatches   15;  Indels    5;  Gaps    1;
```



RESULT 5
AAW90933
ID AAW90933 standard; Protein; 470 AA.
XX
AC AAW90933;
XX
DT 08-AUG-2000 (first entry)
XX
DE Humanised anti Fas designed heavy chain Hcu 1 protein.
XX
KW Fas; antibody; human; anti inflammatory; anti anemic; antidiabetic;
KW anti allergic; anti arthritic; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
PN EP990663-A2.
XX
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY) SANKYO CO LTD.
XX
PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi I;
XX
DR WPI; 2000-256040/23.
DR N-PSDB; AAA11644.
XX
PT New humanized anti Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas Fas ligand systems
XX
PS Claim 2; Page 169-170; 263pp; English.
XX
CC This invention describes a novel humanised anti Fas antibody like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti inflammatory,
CC anti anemic, antidiabetic, anti allergic, anti arthritic, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti Fas antibody heavy chain construct designated Hcu 1
CC which is described in the method of the invention.
XX
SQ Sequence 470 AA;



RESULT 6
ABB74902
ID ABB74902 standard; Protein; 470 AA.
XX
AC ABB74902;
XX
DT 26-APR-2002 (first entry)
XX
DE Humanised anti Fas antibody light chain SEQ ID NO 54.
XX
KW Human; mouse, humanised anti Fas antibody; Fas/Fas ligand;
KW light chain subunit; apoptosis; immunosuppressive; antialiergic;
KW autoimmune disease; allergy; atopic.
XX
OS Synthetic.
XX
PN JP2001342148-A.
XX
PD 11-DEC-2001.
XX
PF 28-MAR-2001; 2001JP-0094106.
XX
PR 29-MAR-2000; 2000JP-0090918.
XX
PA (SANY) SANKYO CO LTD.
XX
DR WPI; 2002-115113/19.
DR N-PSDB; ABL45942.
XX
PT Drug containing humanised anti-Fas antibody, used for preventing and
PT treating autoimmune diseases, allergy, and atopy.
XX
PS Example 14 (Preparatory); Page 96; 194pp; Japanese.
XX
CC The invention relates to a preventive or treating agent for diseases
CC caused by abnormality in Fas/Fas ligand system containing as the active
CC component an antibody having as the light chain subunit a polypeptide
CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,
CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all

```
CC   fully defined in the specification and having an activity of combining
CC   specifically with mammalian Fas and an activity of inducing apoptosis
CC   in a cell expressing Fas. The agent has immunosuppressive and
CC   antiallergic activity and is used for preventing and treating autoimmune
CC   diseases, allergy, atopy and others.
XX
SQ   Sequence   470 AA;

  Query Match             80.9%;  Score 582.5;  DB 23;  Length 470;
  Best Local Similarity   80.7%;  Pred. No. 1.5e-42;
  Matches  113;  Conservative    7;  Mismatches   15;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:||| ||| ||||||||||||||||||||||||||||:|||||||||||| | :|||:|||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKHGASVKVSCKASGYIFISYWMQWVKQAP 60

Qy         61 GQGLEWMGEIDPSDSYINYNQKFKDRVTITVDKSTATMELSSLRSEDTAVYYCARAA  114
              |||||:| :|:     |||||||||||||:||| ||||||||||:|||||||||||
Db         61 GQGLEWMGEIDPSDSYINYNLKFKDKATITVDTSTATMELSSLRSEDTAVYYCARNS  120

Qy        120 ----WYMDYWGQGTLVTVSS 135
                  || | ||||||||||
Db        121 YSNNWYFDVWGQGTLVTVSS 140


RESULT 7
AAW60934
ID   AAW60934 standard; Protein; 470 AA.
XX
AC   AAW60934;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Humanised anti-Fas designed heavy chain Hcm 2 protein.
XX
KW   Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW   antiallergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
KW   dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW   neuroprotective; antiinfertility; neuroprotective; antiarteriosclerotic;
KW   hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW   Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW   Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW   Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW   multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW   insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW   cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS   Synthetic.
XX
PN   EP990663-A2.
XX
PD   05-APR-2000.
XX
PF   29-SEP-1999;   99EP-0307711.
XX
PR   30-SEP-1998;   98JP-0276881.
PR   30-SEP-1998;   98JP-0276882.
XX
PA   (SANY ) SANKYO CO LTD.
XX
PI   Soejima N,  Hatayama H,  Nakahara K,  Tamaki I,  Takahashi I;
XX
DR   WPI; 2000-258940/23.
DR   N-PSDB; AAA11645.
XX
PT   New humanized anti Fas antibody, useful for treating or preventing e.g.
PT   inflammatory or autoimmune disease, induces apoptosis selectively in
PT   cells with abnormal Fas Fas ligand systems
XX
PS   Claim 2 ; Page 174-176; 263pp; English.
XX
CC   This invention describes a novel humanized anti Fas antibody like
CC   molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC   ligand system, by binding to Fas on the cell surface, and prevents
CC   apoptosis in cells with a normal system, by inhibiting binding between
CC   Fas and its ligand. The products of the invention have anti inflammatory,
CC   anti-anemic, antidiabetic, anti-allergic, anti arthritic, antiviral,
CC   immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC   antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC   antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC   apoptosis by binding to cell surface Fas or inhibit it by competitive
CC   inhibition of ligand binding. (I) are used to treat and/or prevent
CC   diseases associated with the Fas/Fas ligand system, especially systemic
CC   lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC   versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC   anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC   disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC   multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC   dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC   cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC   (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC   inhibit apoptosis in normal cells but selectively induce it in abnormal
CC   cells. They bind to both human and murine Fas, so can be evaluated in
CC   murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC   the native ligand, do not induce liver disease, and have reduced risk of
CC   inducing a human anti murine antibody response. This sequence represents
CC   a humanised anti Fas antibody heavy chain construct designated Hcm 2
CC   which is described in the method of the invention.
XX
SQ   Sequence   470 AA;

  Query Match             80.8%;  Score 581.5;  DB 21;  Length 470;
  Best Local Similarity   80.7%;  Pred. No. 1.8e-42;
  Matches  113;  Conservative    7;  Mismatches   15;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:||| ||| ||||||||||||||||||||||||||||:|||||||||||| | :|||:|||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKHGASVKVSCKASGYIFISYWMQWVKQAP 60

Qy         61 GQGLEWMGEIDPSDSYINYNQKFKDRVTITVDKSTATMELSSLRSEDTAVYYCARAA  114
              |||||:| :|:     |||||||||||||:||| ||||||||||:|||||||||||
Db         61 GQGLEWMGEIDPSDSYINYNLKFKDKATITVDTSTATMELSSLRSEDTAVYYCARNS  120

Qy        120     WYMDYWGQGTLVTVSS 135
                  || | ||||||||||
Db        121 YSNNWYFDVWGQGTLVTVSS 140


RESULT 8
ABB74903
ID   ABB74903 standard; Protein; 470 AA.
XX
AC   ABB74903;
XX
DT   26-APR-2002  (first entry)
XX
DE   Mouse humanised anti Fas antibody related protein SEQ ID NO 11.
XX
KW   Human; mouse; humanised anti Fas antibody; Fas/Fas ligand;
KW   light chain subunit; apoptosis; immunosuppressive; antiallergic;
KW   autoimmune disease; allergy; atopic.
XX
OS   Mus musculus.
XX
PN   JP2001342148-A.
XX
PD   11-DEC-2001.
XX
PF   28-MAR-2001;  2001JP-0093106.
XX
PR   29-MAR-2000;  2000JP-0090918.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2002-141113/19.
DR   N-PSDB; ABL45925.
```

```
XX
PT   Drug containing humanised anti Fas antibody, used for preventing and
PT   treating autoimmune diseases, allergy, and atopy
XX
PS   Example 4 (Preparatory); Page 81-82; 194pp; Japanese.
XX
CC   The invention relates to a preventive or treating agent for diseases
CC   caused by abnormality in Fas/Fas ligand system containing as the active
CC   component an antibody having as the light chain subunit a polypeptide
CC   containing residues 1-218 of one of 3, 239 residue amino acid sequences,
CC   or residues 1-451 of one of 3, 470 residue amino acid sequences, all
CC   fully defined in the specification and having an activity of combining
CC   specifically with mammalian Fas and an activity or inducing apoptosis
CC   in a cell expressing Fas. The agent has immunosuppressive and
CC   antiallergic activity and is used for preventing and treating autoimmune
CC   diseases, allergy, atopy and others.
XX
SQ   Sequence   470 AA;

  Query Match             80.8%;  Score 581.5;  DB 23;  Length 470;
  Best Local Similarity   80.7%;  Pred. No. 1.8e-42;
  Matches  113;  Conservative    7;  Mismatches   15;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              ||:|:|| ||| ||||||||||||||||||||||||:|||||||||||| | :|||:|||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60

Qy         61 GQGLEWIGVINTYYGNTNYNQKFKGKAIMIVDKSISTAYMELSSLRSEDTAVYYCARAA- 119
              |||||||:|:     |||||||||||||:||| |||||||||||:|||||||||||||
Db         61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSISTAYMELSSLRSEDTAVYYCARNRD 120

Qy        120      WYMDYWGQGTLVTVSS 135
                   || | ||||||||||||
Db        121 YSNNWYFDVWGQGTLVTVSS 140


RESULT 9
AAW80037
ID   AAW80037 standard; Protein; 470 AA.
XX
AC   AAW80037;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Anti Fas humanised antibody HFE7A heavy chain.
XX
KW   HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW   apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW   systemic lupus erythematosus; graft versus host disease;
KW   Sjogren syndrome; pernicious anaemia; Addison's disease;
KW   scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW   rheumatoid arthritis; autoimmune haemolytic anaemia;
KW   myasthenia gravis; multiple sclerosis; Basedow's disease;
KW   thrombopenia purpura; insulin dependent diabetes; allergy;
KW   atopy; arteriosclerosis; myocarditis, cardiomyopathy,
KW   glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW   transplant rejection; therapy.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= Sig_peptide
FT   Protein         20..470
FT                   /label= Mat_protein
FT   Region          20..140
FT                   /label= Variable
FT   Region          141..464
FT                   /label= Constant
FT   Region          [illegible]..[illegible]94
FT                   /label= CDR_H1
FT                   /note= "claim 9"
FT   Region          69..84
FT                   /label= CDR_H2
FT                   /note= "claim 9"
FT   Region          118..129
FT                   /label= CDR_H3
FT                   /note= "claim 9"
XX
PN   AU9859701-A.
XX
ID   08-OCT-1998.
XX
PF   30-MAR-1998;   98AU-0059701.
XX
PR   08-OCT-1997;   97JP-0276064.
PR   01-APR-1997;   97JP-0082953.
PR   25-JUN-1997;   97JP-0169088.
XX
PA   (SANY ) SANKYO CO LTD.
XX
PI   Akio S,  Hideyuki H,  Hiroko Y,  Jun O,  Kimihisa I;
PI   Masahiko O,  Nobutusa S,  Shin Y,  Tohru T;
XX
DR   WPI; 1998-543440/47.
DR   N-PSDB; AAV70080.
XX
PT   New antibodies and proteins bind conserved epitope of Fas antigen -
PT   used to evaluate drugs in animal models and to treat Fas associated
PT   diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT   myocarditis, hepatitis and AIDS
XX
PS   Claim 22; Page 225-227; 292pp; English.
XX
CC   This is the amino acid sequence of the HV type humanised heavy
CC   chain of murine anti-human Fas monoclonal antibody HFE7A.  It
CC   includes humanising R44G and A76T amino acid substitutions that are
CC   are conserved in the human IgG heavy chain.  Host Escherichia coli
CC   pqHPDHV3 SANK 70298 harbours plasmid pqHPDHV3 carrying a fusion
CC   fragment of the humanised HV type HFE7A heavy chain and DNA
CC   encoding human IgG1 constant region (see AAV70080), and is deposited
CC   as FERM BP-6274 (claimed).  The invention provides methods for
CC   producing humanised antibodies by culturing host cells.  Humanised
CC   versions of HFE7A (see AAW80041-47), like native HFE7A, are capable
CC   of inducing apoptosis in abnormal cells expressing Fas, and of
CC   inhibiting Fas induced apoptosis in normal cells.  The humanised
CC   antibodies are used to evaluate, in animal models, treatments of
CC   diseases that involve Fas/Fas ligand interactions, and also to
CC   treat such diseases, including autoimmune disease (e.g. systemic
CC   lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC   Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC   Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC   autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC   multiple sclerosis, Basedow's disease, thrombopenia purpura and
CC   insulin dependent diabetes), allergies, atopy, arteriosclerosis,
CC   myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC   anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ   Sequence   470 AA;

  Query Match             80.5%;  Score 579.5;  DB 19;  Length 470;
  Best Local Similarity   80.0%;  Pred. No. 2.6e-42;
  Matches  112;  Conservative    8;  Mismatches   15;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              ||:|:|| ||| ||||||||||||||||||||||||:|||||||||||| | :|||:|||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60

Qy         61 GQGLEWIGVINTYYGNTNYNQKFKGKAIMIVDKSISTAYMELSSLRSEDTAVYYCARAA- 119
              |||||||:|:     |||||||||||||:||| |||||||||||:|||||||||||||
Db         61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSISTAYMELSSLRSEDTAVYYCARNRD 120

Qy        120      WYMDYWGQGTLVTVSS 135
                   || | ||||||||||||
Db        121 YSNNWYFDVWGQGTLVTVSS 140
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```
RESULT 10
AAB14779
ID   AAB14779 standard; Protein; 470 AA.
XX
AC   AAB14779;
XX
DT   24-NOV-2000  (first entry)
XX
DE   Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
XX
KW   Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW   murine; humanised antibody; complementarity determining region; CDR;
KW   human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW   autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW   cardiomyopathy; glomerulonephritis; aplastic anaemia; pannyelophthisis;
KW   hepatitis; AIDS; graft rejection; heavy chain.
XX
OS   Chimeric - Mus musculus.
OS   Chimeric - Homo sapiens.
XX
PN   JP2000166553-A.
XX
PD   20-JUN-2000.
XX
PF   30-SEP-1999;   99JP-0278301.
XX
PR   30-SEP-1998;   98JP-0276883.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2000-485645/43.
DR   N-PSDB; AAA72184.
XX
PT   Preventive or treating agent for the diseases caused by an abnormality
PT   in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT   anti Fas antibody
XX
PS   Claim 21; Page 108-109; 136pp; Japanese.
XX
CC   The invention relates to compositions for the prevention or treatment
CC   of diseases caused by an abnormality in the Fas/Fas ligand system
CC   containing an anti-Fas antibody as the active component. The anti Fas
CC   antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC   or a humanised version of HFE7A containing identical CDRs
CC   (complementarity determining regions) to antibody HFE7A. Via its
CC   interaction with Fas, the antibody of the invention acts as a modulator
CC   of apoptosis. The compositions of the invention may therefore be used in
CC   the treatment or prevention of conditions such as autoimmune diseases,
CC   allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC   glomerulonephritis, aplastic anaemia (pannyelophthisis), hepatitis, AIDS
CC   and organ graft rejection. Sequences AAB14775 B14776 and AAB14779
CC   represent the heavy chains (or fragments thereof) of various humanised
CC   HFE7A-derived anti-Fas antibodies.
XX
SQ   Sequence  470 AA;

  Query Match             80.5%;  Score 579.5;  DB 21;  Length 470;
  Best Local Similarity   80.0%;  Pred. No. 2.6e-42;
  Matches  112;  Conservative    8;  Mismatches   15;  Indels    5;  Gaps    1;

Qy          1 MGWSCIILFLVATATGVHSQVQLVQSAEVKKPGSSVKVSCKASGYTFTDYATQWVRQAP 60
              ||:|||| ||| ||||||||||||||||||||||:|||||||||||||| | :|||:|||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60

Qy         61 GQGLEWIGVINIYYDNENNYNQKFKGRATLTVDKSTSTAYMELSSLRSEDTAVYYCARNRD 120
              |||||||:|:|:     ||||||||||||||:||| ||||||||||||||||||||||||
Db         61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLKSEDTAVYYCARNRD 120

Qy        121 ----WYMDYWGQGTLVTVSS 135
                  || | ||:|||||||||
Db        121 YSNNWYFDVWGEGTLVTVSS 140
```

```
RESULT 11
AAW90929
ID   AAW90929 standard; Protein; 470 AA.
XX
AC   AAW90929;
XX
DT   08-AUG-2000  (first entry)
XX
DE   Humanised HFE7A designed heavy chain protein #2.
XX
KW   Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW   anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
KW   dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW   nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW   hepatotropic; humanised; apoptosis; systemic lupus erythematosus;
KW   Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW   Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW   Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW   multiple sclerosis; Basedow's disease; thrombopenia purpura; alopecia;
KW   insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW   cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS   Synthetic.
XX
PN   EP990663-A2.
XX
PD   05-APR-2000.
XX
PF   29-SEP-1999;   99EP-0307711.
XX
PR   30-SEP-1998;   98JP-0276881.
PR   30-SEP-1998;   98JP-0276882.
XX
PA   (SANY ) SANKYO CO LTD.
XX
PI   Serizawa N, Hamuyama H, Nakahara K, Tanaki I, Takahashi T;
XX
DR   WPI; 2000-258930/23.
DR   N-PSDB; AAA11622.
XX
PT   New humanized anti Fas antibody, useful for treating or preventing e.g.
PT   inflammatory or autoimmune disease, induces apoptosis selectively in
PT   cells with abnormal Fas Fas ligand systems
XX
PS   Example reference 22; Page 150-152; 268pp; English.
XX
CC   This invention describes a novel humanized anti-Fas antibody like
CC   molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC   ligand system, by binding to Fas on the cell surface, and prevents
CC   apoptosis in cells with a normal system, by inhibiting binding between
CC   Fas and its ligand. The products of the invention have anti inflammatory,
CC   anti anemic, antidiabetic, anti allergic, anti arthritic, antiviral,
CC   immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC   antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC   antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC   apoptosis by binding to cell surface Fas or inhibit it by competitive
CC   inhibition of ligand binding. (I) are used to treat and/or prevent
CC   diseases associated with the Fas/Fas ligand system, especially systemic
CC   lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC   versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC   anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC   disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC   multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC   dependent diabetes mellitus, alleray, arteriosclerosis, myocarditis,
CC   cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC   (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC   inhibit apoptosis in normal cells but selectively induce it in abnormal
CC   cells. They bind to both human and murine Fas, so can be evaluated in
CC   murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC   the native ligand, do not induce liver disease, and have reduced risk of
CC   inducing a human anti-murine antibody response. This sequence represents
```

CC a humanised anti Fas antibody HFE7A derived heavy chain which is used in
CC the method described in the invention.
XX
SQ Sequence 470 AA;

Query Match 80.5%; Score 579.5; DB 23; Length 470;
Best Local Similarity 80.0%; Pred. No. 2.6e-42;
Matches 112; Conservative 8; Mismatches 15; Indels 5; Gaps 1;

Qy 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWMQWVKQAP 60
||:|||| ||| |||||||||||||||||||||||||||||||| | :|||:|||
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFKGKATMIVDKSISTAYMELSSLRSEDTAVYYCARAA- 119
|||||||: |: ||||||||||||:||| |||||||||||||||||||||||
Db 61 GQGLEWMGEIDPSDSYINYNQKFKGKATLIVDTSISTAYMELSSLRSEDTAVYYCARNKD 120

Qy 120 WYMDYWGQGTLVTVSS 135
|| | ||:||||||||
Db 121 YSNNWYFDVWGEGTLVTVSS 140

RESULT 12
ABB74808
ID ABB74808 standard; Protein; 470 AA.
XX
AC ABB74808;
XX
DT 29-APR-2002 (first entry)
XX
DE Humanised anti Fas antibody light chain SEQ ID NO 129.
XX
KW Human; mouse; humanised anti Fas antibody; Fas/Fas ligand;
KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
KW autoimmune disease; allergy; atopic.
XX
OS Synthetic.
XX
PN JP2001342148-A.
XX
PD 11-DEC-2001.
XX
PF 28-MAR-2001; 2001JP-0093106.
XX
PR 29-MAR-2000; 2000JP-0089018.
XX
PA (SANY) SANKYO CO LTD.
XX
DR WPI; 2002-145113/19.
DR N-PSDB; ABL49038.
XX
PT Drug containing humanised anti Fas antibody, used for preventing and
PT treating autoimmune diseases, allergy, and atopy
XX
PS Claim 1; Page 131-132; 194pp; Japanese.
XX
CC The invention relates to a preventive or treating agent for diseases
CC caused by abnormality in Fas/Fas ligand system containing as the active
CC component an antibody having as the light chain subunit a polypeptide
CC containing residues 1-218 of one of 5, 239 residue amino acid sequences,
CC or residues 1-451 of one of 8, 470 residue amino acid sequences, all
CC fully defined in the specification and having an activity of combining
CC specifically with mammalian Fas and an activity of inducing apoptosis
CC in a cell expressing Fas. The agent has immunosuppressive and
CC antiallergic activity and is used for preventing and treating autoimmune
CC diseases, allergy, atopy and others.
XX
SQ Sequence 470 AA;

Query Match 80.5%; Score 579.5; DB 23; Length 470;
Best Local Similarity 80.0%; Pred. No. 2.6e-42;
Matches 112; Conservative 8; Mismatches 15; Indels 5; Gaps 1;

Qy 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWMQWVKQAP 60
||:|||| ||| |||||||||||||||||||||||||||||||| | :|||:|||
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFKGKATMIVDKSISTAYMELSSLRSEDTAVYYCARAA- 119
|||||||: |: ||||||||||||:||| |||||||||||||||||||||||
Db 61 GQGLEWMGEIDPSDSYINYNQKFKGKATLIVDTSISTAYMELSSLRSEDTAVYYCARNKD 120

Qy 120 WYMDYWGQGTLVTVSS 135
|| | ||:||||||||
Db 121 YSNNWYFDVWGEGTLVTVSS 140

RESULT 13
ABB74944
ID ABB74944 standard; Protein; 470 AA.
XX
AC ABB74944;
XX
DT 30-APR-2002 (first entry)
XX
DE Humanised anti-Fas antibody related polypeptide SEQ ID NO 11.
XX
KW Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;
KW heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;
KW autoimmune disease; allergy; atopy.
XX
OS Mus musculus.
XX
PN JP2001342149-A.
XX
PD 11-DEC-2001.
XX
PF 28-MAR-2001; 2001JP-0093243.
XX
PR 29-MAR-2000; 2000JP-0091144.
XX
PA (SANY) SANKYO CO LTD.
XX
DR WPI; 2002-145111/19.
DR N-PSDB; ABL48758.
XX
PT Drug for preventing or treating e.g. autoimmune disease or allergy,
PT comprises humanised anti Fas antibody
XX
PS Example 4 (preparatory); Page 70; 154pp; Japanese.
XX
CC The invention relates to a preventive or treating agent for diseases
CC caused by abnormality in the Fas/Fas ligand system containing, as the
CC active component, an antibody having a light chain subunit and a heavy
CC chain subunit and an activity of combining specifically with mammalian
CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The
CC agent has antiallergic, immunosuppressive and apoptotic activity and is
CC used for preventing and treating autoimmune diseases, allergy, atopy and
CC others.
XX
SQ Sequence 470 AA;

Query Match 80.5%; Score 579.5; DB 23; Length 470;
Best Local Similarity 80.0%; Pred. No. 2.6e-42;
Matches 112; Conservative 8; Mismatches 15; Indels 5; Gaps 1;

Qy 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWMQWVKQAP 60
||:|||| ||| |||||||||||||||||||||||||||||||| | :|||:|||
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFKGKATMIVDKSISTAYMELSSLRSEDTAVYYCARAA- 119
|||||||: |: ||||||||||||:||| |||||||||||||||||||||||
Db 61 GQGLEWMGEIDPSDSYINYNQKFKGKATLIVDTSISTAYMELSSLRSEDTAVYYCARNKD 120

Qy 120 WYMDYWGQGTLVTVSS 135
|| | ||:||||||||
Db 121 YSNNWYFDVWGEGTLVTVSS 140

RESULT 14
AAR55556
ID AAR55556 standard; Protein; 140 AA.
XX
AC AAR55556;
XX
DT 15-NOV-1994 (first entry)
XX
DE DREG 200 humanized antibody heavy chain variable region.
XX
KW DREG-200; L-selectin; LECAM-1; Mel-14; LAM-1;
KW humanized antibody; immunoglobulin; Ig; IgG1; Ig64;
KW complementarity determining region; CDR; monoclonal antibody; MAb;
KW framework; light chain; heavy chain; variable domain;
KW monoclonal antibody; acceptor antibody Eu; transgenic animal.
XX
OS Mus sp.; Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Region 50..54
FT /label= CDR1
FT Region 69..85
FT /label= CDR2
FT Region 118..129
FT /label= CDR3
XX
PN WO9412215-A.
XX
PD 09-JUN-1994.
XX
PF 30-NOV-1993; 93WO-US11612.
XX
PR 01-DEC-1992; 92US-0983946.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Co MS;
XX
DR WPI; 1994-199974/24.
DR N-PSDB; AAQ66702.
XX
PT New humanised antibody specific for L-selectin - with murine CDR
PT and human framework regions, inhibits binding of neutrophils to
PT endothelial cells and useful for treating or preventing
PT inflammation
XX
PS Disclosure; Fig. 3B; 60pp; English.
XX
CC An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs
CC corresponding to those of mouse MAb DREG-200 and heavy and light
CC chain variable region frameworks of the human acceptor antibody Eu.
CC Nucleotide and aa sequences are provided for the DREG 200 light
CC (AAQ66699, AAR55553) and heavy (AAQ66700, AAR55554) chain variable
CC regions and the humanized DREG-200 light (AAQ66701, AAR55555) and heavy
CC (AAQ66702, AAR55556) chain variable regions. The humanized antibodies
CC can be produced economically in large quantities by expression in
CC mammalian cell culture or in transgenic animals.
XX
SQ Sequence 140 AA;

Query Match 79.7%; Score 573.5; DB 15; Length 140;
Best Local Similarity 78.6%; Pred. No. 2.5e-42;
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

Qy 1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
|:|:||| ||| ||||||||||||||||||||||||||||||||||||||| | : ||||||
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYVVQWVRQAP 60

Qy 61 GQGLEWIGYIYPYNDGTKYNEKFKGRVTITSDESTNTAYMELSSLRSEDTAVYYCAREEY 120

Qy 121 -----YMDYWGQGTLVTVSS 140
| | ||||||||||
Db 121 GNYVRYTPVWFGQGTLVTVSS 140

RESULT 15
AAW90946
ID AAW90946 standard; Protein; 470 AA.
XX
AC AAW90946;
XX
DT 08-AUG-2000 (first entry)
XX
DE Humanised BFE7A designed heavy chain HHH type protein.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanised; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
PN EP990663-A2.
XX
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY-) SANKYO CO LTD.
XX
PI Serizawa N, Hiroyama M, Nakabeya R, Tamaki T, Tokahashi T;
XX
DR WPI; 2000-276450/23.
DR N-PSDB; AAA11655.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
XX
PS Claim 2; Page 188-189; 263pp; English.
XX
CC This invention describes a novel humanized anti-Fas antibody (Ab)
CC selective (I) that induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting the interaction
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

```
;**   (B, C or D) or alcoholic), and transplant rejection. (1) selectively
;**   inhibit apoptosis in normal cells but selectively induce it in abnormal
;**   cells. They bind to both human and murine Fas, so can be evaluated in
;**   murine disease models. (1) act on the active site of Fas, i.e. they mimic
;**   the native ligand, do not induce liver disease, and have reduced risk of
;**   inducing a human anti murine antibody response. This sequence represents
;**   a humanised anti Fas antibody HFE7A heavy chain construct HHH type
;**   which is described in the method of the invention.
XX
SQ   Sequence   470 AA;

  Query Match             78.8%;  Score 567.5;  DB 21;  Length 470;
  Best Local Similarity   78.6%;  Prod. No. 2.7e-41;
  Matches  110;  Conservative    8;  Mismatches   17;  Indels    5;  Gaps    1;

Qy           1 MGWNCIIFFLVIIATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIQWVRQAP 60
               ||:|:|: ||| |||||||||||||||||||||||:|||||||||||||||| | :|||||||
Db           1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAP 60

Qy          61 GQGLEWIGVINTYYDNTNYNQKFKGKAIMTVDKSTSTAYMELSSLRSEDTAVYYCAKAA- 119
               |||||:| |:     |||||||||: |:    ||||||||||||||||||||||||
Db          61 GQGLEWMGEIDPSDSYTNYNQKFKGRVTITRDTSISTAYMELSSLRSEDTAVYYCARNKD 120

Qy         120      WYMDYWGQGTLVTVSS 135
                    |: | ||:|||||||
Db         121 YSNNWYFDVWGEGTLVTVSS 140


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Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	720	100.0	461	9	US-09-249-011A-24	Sequence 24, Appl
3	627	87.1	135	9	US-09-249-011A-2	Sequence 2, Appli
4	585.5	81.3	470	9	US-10-216-484-147	Sequence 147, App
5	582.5	80.9	470	9	US-10-216-484-143	Sequence 143, App
6	581.5	80.8	470	9	US-10-216-484-145	Sequence 145, App
7	579.5	80.5	470	9	US-10-216-484-117	Sequence 117, App
8	567.5	78.8	470	9	US-10-216-484-157	Sequence 157, App
9	566.5	78.7	145	9	US-10-216-484-75	Sequence 75, Appl
10	566.5	78.7	470	9	US-10-216-484-89	Sequence 89, Appl
11	547	76.0	515	10	US-09-825-012-66	Sequence 66, Appl
12	547	76.0	517	10	US-09-825-012-38	Sequence 38, Appl
13	547	76.0	519	10	US-09-825-012-76	Sequence 76, Appl
14	547	76.0	519	10	US-09-825-012-80	Sequence 80, Appl
15	547	76.0	521	10	US-09-825-012-71	Sequence 71, Appl
16	547	76.0	525	10	US-09-825-012-85	Sequence 85, Appl
17	547	76.0	527	10	US-09-825-012-43	Sequence 43, Appl
18	547	76.0	529	10	US-09-825-012-95	Sequence 95, Appl
19	547	76.0	531	10	US-09-825-012-90	Sequence 90, Appl
20	547	76.0	729	10	US-09-825-012-52	Sequence 52, Appl
21	547	76.0	730	10	US-09-825-012-49	Sequence 49, Appl
22	547	76.0	731	10	US-09-825-012-46	Sequence 46, Appl
23	547	76.0	739	10	US-09-825-012-61	Sequence 61, Appl
24	547	76.0	740	10	US-09-825-012-58	Sequence 58, Appl
25	547	76.0	741	10	US-09-825-012-55	Sequence 55, Appl
26	530.5	73.7	136	9	US-10-160-232-91	Sequence 91, Appl
27	530.5	73.7	140	9	US-10-283-349-63	Sequence 63, Appl
28	528.5	73.4	464	9	US-10-216-484-9	Sequence 9, Appli
29	527	73.2	139	9	US-09-269-921-125	Sequence 125, App
30	527	73.2	139	9	US-09-509-098-50	Sequence 50, Appl
31	527	73.2	139	10	US-09-760-723-7	Sequence 7, Appli
32	527	73.2	139	10	US-09-355-925-7	Sequence 7, Appli
33	526	73.1	139	9	US-09-269-921-111	Sequence 111, App
34	526	73.1	139	9	US-09-509-098-22	Sequence 22, Appl
35	523	72.6	139	9	US-09-269-921-110	Sequence 110, App
36	523	72.6	139	9	US-09-269-921-128	Sequence 128, App
37	523	72.6	139	9	US-09-509-098-20	Sequence 20, Appl
38	523	72.6	139	9	US-09-509-098-127	Sequence 127, App
39	523	72.6	139	10	US-09-760-723-8	Sequence 8, Appli
40	523	72.6	139	10	US-09-355-925-8	Sequence 8, Appli
41	522.5	72.6	180	10	US-09-748-960-6	Sequence 6, Appli
42	521	72.4	139	9	US-09-269-921-117	Sequence 117, App
43	521	72.4	139	9	US-09-269-921-123	Sequence 123, App
44	521	72.4	139	9	US-09-509-098-34	Sequence 34, Appl
45	521	72.4	139	9	US-09-509-098-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-09-249-011A-6
; Sequence 6, Application US/09249011A
Patent No. US20020176855A1
GENERAL INFORMATION:
APPLICANT: QU, HAN ZHONG
APPLICANT: VAZQUEZ, MAXIMILIANO
APPLICANT: CAMPOCH, BEATRIZ
APPLICANT: CELNIKER, ABBIE CHERYL
APPLICANT: COLLINS, MARY
APPLICANT: GOLDMAN, SAMUEL
APPLICANT: GRAY, GARY S.
APPLICANT: KNIGHT, ANDREA
APPLICANT: O'HARA, DENISE
APPLICANT: RUP, BONITA
APPLICANT: VELDMAN, GEERTRUIDA M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7.2 AND METHODS
TITLE OF INVENTION: OF TREATMENT THEREWITH
FILE REFERENCE: 08702.0081-00000
CURRENT APPLICATION NUMBER: US/09/249,011A
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 135
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Humanized
OTHER INFORMATION: murine anti-human B7.2 heavy chain
US-09-249-011A-6

Query Match 100.0%; Score 720; DB 9; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.9e-51;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60

Qy         61 GQGLEWIGVINTYYPNTNYNQKFKGRATMTVDKSISTAYMELSRLRSDDTAVYYCARAAW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Db          61 GQGLEWIGVINIYYDNINYNQKFKGKATMIVDKSSSTAYMELSSLRSEDTAVYYCARAAW 120

Qy         121 YMDYWGQGTLVTVSS 135
               ||||||||||||||||
Db         121 YMDYWGQGTLVTVSS 135


RESULT 2
US-09-249-011A-24
; Sequence 24, Application US/09249011A
; Patent No. US20020176859A1
; GENERAL INFORMATION:
;  APPLICANT: CO, MAN SUNG
;  APPLICANT:  VASQUEZ, MAXIMILIANO
;  APPLICANT:  CARRENO, BEATRIZ
;  APPLICANT:  CELNIKER, ABBIE CHERYL
;  APPLICANT:  COLLINS, MARY
;  APPLICANT:  GOLDMAN, SAMUEL
;  APPLICANT:  GRAY, GARY S.
;  APPLICANT:  KNIGHT, ANDREA
;  APPLICANT:  O'HARA, DENISE
;  APPLICANT:  RUP, BONITA
;  APPLICANT:  VELDMAN, GEERTRUIDA M.
;  TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
;  TITLE OF INVENTION:  OF TREATMENT THEREWITH
;  FILE REFERENCE: 08702.0081-00000
;  CURRENT APPLICATION NUMBER: US/09/249,011A
;  CURRENT FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;  LENGTH: 461
;  TYPE: PRT
;  ORGANISM: Mus sp.
US-09-249-011A-24

  Query Match             100.0%;  Score 720;  DB 9;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-50;
  Matches  135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60

Qy          61 GQGLEWIGVINIYYDNINYNQKFKGKATMIVDKSSSTAYMELSSLRSEDTAVYYCARAAW 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GQGLEWIGVINIYYDNINYNQKFKGKATMIVDKSSSTAYMELSSLRSEDTAVYYCARAAW 120

Qy         121 YMDYWGQGTLVTVSS 135
               |||||||||||||||
Db         121 YMDYWGQGTLVTVSS 135


RESULT 3
US-09-249-011A-2
; Sequence 2, Application US/09249011A
; Patent No. US20020176859A1
; GENERAL INFORMATION:
;  APPLICANT: CO, MAN SUNG
;  APPLICANT:  VASQUEZ, MAXIMILIANO
;  APPLICANT:  CARRENO, BEATRIZ
;  APPLICANT:  CELNIKER, ABBIE CHERYL
;  APPLICANT:  COLLINS, MARY
;  APPLICANT:  GOLDMAN, SAMUEL
;  APPLICANT:  GRAY, GARY S.
;  APPLICANT:  KNIGHT, ANDREA
;  APPLICANT:  O'HARA, DENISE
;  APPLICANT:  RUP, BONITA
;  APPLICANT:  VELDMAN, GEERTRUIDA M.
;  TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
;  TITLE OF INVENTION:  OF TREATMENT THEREWITH
;  FILE REFERENCE: 08702.0081-00000
;  CURRENT APPLICATION NUMBER: US/09/249,011A
;  CURRENT FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;  LENGTH: 135
;  TYPE: PRT
;  ORGANISM: Murine sp.
;  FEATURE:
;  OTHER INFORMATION: Anti B7-2 heavy chain
US-09-249-011A-2

  Query Match             87.1%;  Score 627;  DB 9;  Length 135;
  Best Local Similarity   84.4%;  Pred. No. 1.2e-43;
  Matches  114;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy           1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
               |||||||||||||||||||||||| ||| |: :|| |||:||| ||||||||||||:|:
Db           1 MGWNCIIFFLVTTATGVHSQVQLQQSGPELVRPGESVKISCKGSGYTFTDYAIQWVKQSH 60

Qy          61 GQGLEWIGVINIYYDNINYNQKFKGKATMIVDKSSSTAYMELSSLRSEDTAVYYCARAAW 120
               : ||||||||||||||||||||||||||||||||||||:|||||| | |||:|||||||||
Db          61 AKSLEWIGVINIYYDNINYNQKFKGKATMIVDKSSSTAYMELARLISEDSAIYYCARAAW 120

Qy         121 YMDYWGQGTLVTVSS 135
               |||||||||| |||||
Db         121 YMDYWGQGTSVTVSS 135


RESULT 4
US-10-216-484-147
; Sequence 147, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976A1tutusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 9801260IP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/058,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 147
;  LENGTH: 470
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
;  OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-147

  Query Match             81.3%;  Score 585.5;  DB 9;  Length 470;
  Best Local Similarity   81.4%;  Pred. No. 9e-40;
  Matches  114;  Conservative    6;  Mismatches   15;  Indels    5;  Gaps    1;

Qy           1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
               |||:||| ||| |||||||||||||||||||||||:|||||||||||||| | :|||||||
Db           1 MGWSCIILFLVATATGVHSQVQLVQSGAEVEKPGASVKVSCKASGYTFTSYWMQWVRQAP 60

Qy          61 GQGLEWIGVINIYYDNINYNQKFKGKATMIVDKSSSTAYMELSSLRSEDTAVYYCARAA 119
               |||||||: |:    ||||||||||||||:||| ||||||||||||||||||||||||
Db          61 GQGIEWMGEINPSDSVTNYNQKFKGRATLTVDTSTSTAYMELSSLRSEDTAVYYCARND 120

Qy         120  --=WYMDYWGQGTLVTVSS 135
                  || | ||||||||||||
Db         121 YSNNWYFDVWGQGTLVTVSS 140
```

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RESULT 5
US-10-216-484-143
; Sequence 143, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976Alutusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 143
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
;   OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-143

  Query Match             80.9%;  Score 582.5;  DB 9;  Length 470;
  Best Local Similarity   80.7%;  Pred. No. 1.6e-39;
  Matches  113;  Conservative    7;  Mismatches   15;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:||| ||| ||||||||||||||||||||||||:|||||||||||| | :|||:|||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

Qy         61 GQGLEWIGVINIYYDNTNYNQKFKGKAIMTVDKSTSTAYMELSSLRSEDTAVYYCARAA- 119
              |||||:| |:     ||||||||||||:||| ||||||||||||||||||||||||||
Db         61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120

Qy        120 ----WYMDYWGQGTLVTVSS 135
                  || | ||||||||||
Db        121 YSNNWYFDVWGQGTLVTVSS 140


RESULT 6
US-10-216-484-145
; Sequence 145, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976Alutusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 145
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
;   OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-145

  Query Match             80.8%;  Score 581.5;  DB 9;  Length 470;
  Best Local Similarity   80.7%;  Pred. No. 1.9e-39;
  Matches  113;  Conservative    7;  Mismatches   15;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:||| ||| ||||||||||||||||||||||||:|||||||||||| | :|||:|||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

Qy         61 GQGLEWIGVINIYYDNTNYNQKFKGKAIMTVDKSTSTAYMELSSLRSEDTAVYYCARAA- 119
              |||||:| |:     ||||||||||||:||| ||||||||||||||||||||||||||
Db         61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120

Qy        120 ----WYMDYWGQGTLVTVSS 135
                  || | ||||||||||
Db        121 YSNNWYFDVWGQGTLVTVSS 140


RESULT 7
US-10-216-484-117
; Sequence 117, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976Alutusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 117
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
;   OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-117

  Query Match             80.5%;  Score 579.5;  DB 9;  Length 470;
  Best Local Similarity   80.0%;  Pred. No. 2.7e-39;
  Matches  112;  Conservative    8;  Mismatches   15;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:||| ||| ||||||||||.||||||||||||:|||||||||||| | :|||:|||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

Qy         61 GQGLEWIGVINIYYDNTNYNQKFKGKAIMTVDKSTSTAYMELSSLRSEDTAVYYCARAA- 119
              |||||:| |:     ||||||||||||:||| ||||||||||||||||||||||||||
Db         61 GQGLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDTAVYYCARNRD 120

Qy        120 --  WYMDYWGQGTLVTVSS 135
                  || | ||:|||||||||
Db        121 YSNNWYFDVWGEGTLVTVSS 140


RESULT 8
US-10-216-484-157
; Sequence 157, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976Alutusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
```

```
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 157
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed
;   OTHER INFORMATION: heavy chain of humanized anti-Fas antibody
US-10-216-484-157

  Query Match             78.8%;  Score 567.5;  DB 9;  Length 470;
  Best Local Similarity   78.6%;  Pred. No. 2.5e-38;
  Matches  110;  Conservative    8;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:|||| ||| ||||||||||||||||||||||||||||:|||||||||||| | ||||||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

Qy         61 GQGLEWIGVINIYYGNTNYNQKFKGKAIMIVDKSTSTAYMELSSLRSEDTAVYYCARAA- 119
              |||||||| |:      ||||||||| ||| | ||||||||||||||||||||||||||
Db         61 GQRLEWMGEIDPSDSYTNYNQKFKGRVTITKDTSTSTAYMELSSLRSEDTAVYYCARNRD 120

Qy        120      WYMDYWGQGTLVTVSSS 145
                   || | |||:|||||||
Db        121 YSNNWYFDVWGEGTLVTVSSS 140


RESULT 9
US-10-216-484-75
; Sequence 75, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976Alufusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti Fas Antibodies
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 75
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed partial
;   OTHER INFORMATION: peptide of the heavy chain of humanized anti-human
;   OTHER INFORMATION: Fas antibody
US-10-216-484-75

  Query Match             78.7%;  Score 566.5;  DB 9;  Length 145;
  Best Local Similarity   78.6%;  Pred. No. 9.6e-39;
  Matches  110;  Conservative    8;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:|||| ||| ||||||||||||||||||||||||||||:|||||||||||| | ||||||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

Qy         61 GQGLEWIGVINIYYGNTNYNQKFKGKAIMIVDKSTSTAYMELSSLRSEDTAVYYCARAA- 119
              |||||||| |:      ||||||||| ||| | ||||||||||||||||||||||||||
Db         61 GQRLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120

Qy        120      WYMDYWGQGTLVTVSSS 145
                   || | |||:|||||||
Db        121 YSNNWYFDVWGEGTLVTVSSS 140


RESULT 10
US-10-216-484-89
; Sequence 89, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976Alufusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 89
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
;   OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-89

  Query Match             78.7%;  Score 566.5;  DB 9;  Length 470;
  Best Local Similarity   78.6%;  Pred. No. 3.1e-38;
  Matches  110;  Conservative    8;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              |||:|||| ||| ||||||||||||||||||||||||||||:|||||||||||| | ||||||
Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

Qy         61 GQGLEWIGVINIYYGNTNYNQKFKGKAIMIVDKSTSTAYMELSSLRSEDTAVYYCARAA- 119
              |||||||| |:      ||||||||| ||| | ||||||||||||||||||||||||||
Db         61 GQRLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120

Qy        120      WYMDYWGQGTLVTVSSS 145
                   || | |||:|||||||
Db        121 YSNNWYFDVWGEGTLVTVSSS 140


RESULT 11
US-09-825-012-66
; Sequence 66, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Robert
;  TITLE OF INVENTION: Compounds for Targeting
;  FILE REFERENCE: 43191 256808
;  CURRENT APPLICATION NUMBER: US/09/825,012
;  CURRENT FILING DATE:  2001-04-04
;  PRIOR APPLICATION NUMBER: US 60/237,159
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: GB 0008049.9
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 515
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

; OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion
US-09-825-012-66

Query Match 76.0%; Score 547; DB 10; Length 515;
Best Local Similarity 76.8%; Pred. No. 1.2e-36;
Matches 106; Conservative 14; Mismatches 14; Indels 4; Gaps 2;

Qy 1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFEGKAIMIVDKSTSTAYMELSSLRSEDTAVYYCARA-- 118
Db 61 GKGLEWVGEILPGSNNSKYNEKFKGKVTIEDTSTNTAYMELSSLRSEDTAVYYCARSYD 120

Qy 119 -AWYMDYWGQGTLVTVSS 135
Db 121 FAWFA-YWGQGTLVTVSS 137

RESULT 12
US-09-825-012-38
; Sequence 38, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion
US-09-825-012-38

Query Match 76.0%; Score 547; DB 10; Length 517;
Best Local Similarity 76.8%; Pred. No. 1.2e-36;
Matches 106; Conservative 14; Mismatches 14; Indels 4; Gaps 2;

Qy 1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
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Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFEGKAIMIVDKSTSTAYMELSSLRSEDTAVYYCARA-- 118
Db 61 GKGLEWVGEILPGSNNSKYNEKFKGKVTIEDTSTNTAYMELSSLRSEDTAVYYCARSYD 120

Qy 119 -AWYMDYWGQGTLVTVSS 135
Db 121 FAWFA-YWGQGTLVTVSS 137

RESULT 13
US-09-825-012-76
; Sequence 76, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion
US-09-825-012-76

Query Match 76.0%; Score 547; DB 10; Length 519;
Best Local Similarity 76.8%; Pred. No. 1.3e-36;
Matches 106; Conservative 14; Mismatches 14; Indels 4; Gaps 2;

Qy 1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFEGKAIMIVDKSTSTAYMELSSLRSEDTAVYYCARA-- 118
Db 61 GKGLEWVGEILPGSNNSKYNEKFKGKVTIEDTSTNTAYMELSSLRSEDTAVYYCARSYD 120

Qy 119 -AWYMDYWGQGTLVTVSS 135
Db 121 FAWFA-YWGQGTLVTVSS 137

RESULT 14
US-09-825-012-80
; Sequence 80, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion
US-09-825-012-80

Query Match 76.0%; Score 547; DB 10; Length 519;
Best Local Similarity 76.8%; Pred. No. 1.3e-36;
Matches 106; Conservative 14; Mismatches 14; Indels 4; Gaps 2;

Qy 1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60
Db 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFEGKAIMIVDKSTSTAYMELSSLRSEDTAVYYCARA-- 118
Db 61 GKGLEWVGEILPGSNNSKYNEKFKGKVTIEDTSTNTAYMELSSLRSEDTAVYYCARSYD 120

Qy 119 -AWYMDYWGQGTLVTVSS 135
Db 121 FAWFA-YWGQGTLVTVSS 137

RESULT 15
US-09-825-012-71
; Sequence 71, Application US/09825012

; Patent No. US20010227080A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43197 256808
; CURRENT APPLICATION NUMBER: US/09/825,011
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,199
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised BMPG1 Fd DNase I fusion
US-09-825-011-71

Query Match 76.0%; Score 547; DB 10; Length 521;
Best Local Similarity 76.8%; Pred. No. 1.3e-36;
Matches 106; Conservative 14; Mismatches 14; Indels 4; Gaps 2;

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Db          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSAYWIEWVRQAP 60

Qy         61 GQGLEWIGVINTYYDNINYNQKFMGRAIMTVDKSISTAYMELSSLRSEDTAVYYCARA-- 118
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Db         61 GKCLEWVCEILPGSNNSRYNEKFKGRVIVTRDISFNTAYMELSSLRSEDIAVYYCARSYD 120

Qy        119 AWYMDYWGQGILVIVSS 135
                |:  ||||||||||||
Db        121 FAWFA YWGQGILVIVSS 137
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Search completed: June 14, 2003, 15:15:14
Job time : 19.2022 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 15:07:46 ; Search time 17.6006 Seconds
(without alignments)
224.455 Million cell updates/sec

Title: US-09-249-011B-6
Perfect score: 720
Sequence: 1 MGWNCIIFFLVTIATGVHSQ.....ARAAWYMSYWSQGTLVTVSS 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	573.5	79.7	140	4	US-08-579-478A-12	Sequence 12, Appl
2	573.5	79.7	140	5	PCT-US93-11612-12	Sequence 12, Appl
3	545	75.7	135	1	US-07-634-278-19	Sequence 19, Appl
4	545	75.7	135	1	US-08-477-728-19	Sequence 19, Appl
5	545	75.7	135	1	US-08-474-040-19	Sequence 19, Appl
6	545	75.7	135	1	US-08-487-200-19	Sequence 19, Appl
7	545	75.7	135	2	US-08-303-969B-31	Sequence 31, Appl
8	545	75.7	135	4	US-08-484-537-19	Sequence 19, Appl
9	541.5	75.8	168	5	PCT-US91-02942-5	Sequence 5, Appli
10	540.5	75.7	140	3	US-08-836-561-63	Sequence 63, Appl
11	540	75.6	467	2	US-07-916-098A-45	Sequence 45, Appl
12	529.5	73.5	136	5	PCT-US93-11611-11	Sequence 11, Appl
13	529.5	73.5	138	3	US-08-513-968-44	Sequence 44, Appl
14	529	73.5	139	2	US-08-656-586-8	Sequence 8, Appli
15	527	73.2	135	1	US-08-142-117B-102	Sequence 102, App
16	527	73.2	135	2	US-08-436-717-102	Sequence 102, App
17	526	73.1	133	4	US-08-219-423A-8	Sequence 8, Appli
18	526	73.1	133	4	US-09-587-526-8	Sequence 8, Appli
19	525	72.9	139	1	US-08-253-877-19	Sequence 19, Appl
20	525	72.9	139	2	US-08-452-164A-19	Sequence 19, Appl
21	525	72.9	139	3	US-08-603-024-18	Sequence 18, Appl
22	521	72.4	135	1	US-08-142-117B-100	Sequence 100, App
23	521	72.4	135	2	US-08-436-717-100	Sequence 100, App
24	521	72.4	137	3	US-08-513-968-38	Sequence 38, Appl
25	518.5	72.0	140	3	US-08-836-561-74	Sequence 74, Appl
26	515.5	71.6	140	3	US-08-836-561-78	Sequence 78, Appl
27	515	71.5	135	1	US-08-142-117B-112	Sequence 112, App
28	515	71.5	135	2	US-08-436-717-112	Sequence 112, App
29	511.5	71.0	136	4	US-08-525-539A-63	Sequence 63, Appl
30	508.5	70.6	143	1	US-08-236-520-7	Sequence 7, Appli
31	508.5	70.6	143	5	PCT-US95-05262-7	Sequence 7, Appli
32	507.5	70.5	140	3	US-08-836-561-84	Sequence 84, Appl
33	506	70.3	472	4	US-09-381-544-4	Sequence 4, Appl
34	504.5	70.1	136	4	US-09-450-524-8	Sequence 8, Appli
35	504.5	69.9	140	1	US-07-946-421-28	Sequence 28, Appl
36	501.5	69.7	123	1	US-08-482-882-53	Sequence 53, Appl
37	501.5	69.7	123	2	US-08-483-389-53	Sequence 53, Appl
38	501.5	69.7	123	2	US-08-487-118D-53	Sequence 53, Appl
39	501.5	69.7	123	2	US-08-473-503-53	Sequence 53, Appl
40	501.5	69.7	123	2	US-08-483-932-53	Sequence 53, Appl
41	501.5	69.7	123	2	US-08-720-420A-53	Sequence 53, Appl
42	501.5	69.7	123	3	US-08-714-017-53	Sequence 53, Appl
43	501.5	69.7	123	3	US-08-475-680-53	Sequence 53, Appl
44	500.5	69.5	142	2	US-08-476-176B-14	Sequence 14, Appl
45	500.5	69.5	142	3	US-08-127-721A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-579-478A-12
; Sequence 12, Application US/08579478A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,478A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114596.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joan D.
; REGISTRATION NUMBER: 32,576
; REFERENCE/DOCKET NUMBER: 15223-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-579-478A-12

  Query Match             79.7%;  Score 574.5;  DB 4;  Length 140;
  Best Local Similarity   78.6%;  Prod. No. 4.2e-50;
  Matches  110;  Conservative    8;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVIIATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIQWVRQAP 60
              ||| ||| ||| ||||||||||||||||||||||||||||||||||||||| | : ||||||
Db          1 MGWSCIILFLVAIATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTSYVMHWVRQAP 60

Qy         61 GQGLEWIGVINIYYYDNINYNQKFEGKATMIVDKSISTAYMELSSLRSEDTAVYYCARAAW 120
              |||||||| | | | | ||:|||| ;:| |||:|||||||||||||||||||||||  :
Db         61 GQGLEWIGYIYPYNGGTKYNEKFKGRVTITSDESTNTAYMELSSLRSEDTAVYYCAREEY 120

Qy        121       YMDYWGQGTLVIVSS 135
                    | | |||||||||||
Db        121 GNYVRYFFDVWGQGTLVIVSS 140


RESULT 2
PCT-US93-11612-12
; Sequence 12, Application PC/TUS9311612
;  GENERAL INFORMATION:
;     APPLICANT:  Co, Man Sung
;     TITLE OF INVENTION:  Humanized Antibodies Reactive with
;     TITLE OF INVENTION:  L-Selectin
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend Khourie and Crew
;       STREET:  One Market Plaza, Steuart Tower, Suite 2000
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/11612
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/983,946
;       FILING DATE:  01-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William M.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  11823-22
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  140 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US93-11612-12

  Query Match             79.7%;  Score 574.5;  DB 5;  Length 140;
  Best Local Similarity   78.6%;  Prod. No. 4.2e-50;
  Matches  110;  Conservative    8;  Mismatches   17;  Indels    5;  Gaps    1;

Qy          1 MGWNCIIFFLVIIATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIQWVRQAP 60
              ||| ||| ||| ||||||||||||||||||||||||||||||||||||||| | : ||||||
Db          1 MGWSCIILFLVAIATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTSYVMHWVRQAP 60

Qy         61 GQGLEWIGVINIYYYDNINYNQKFEGKATMIVDKSISTAYMELSSLRSEDTAVYYCARAAW 120
              |||||||| | | | ||:|||| ;:| |||:|||||||||||||||||||||||  :
Db         61 GQGLEWIGYIYPYNGGTKYNEKFKGRVTITSDESTNTAYMELSSLRSEDTAVYYCAREEY 120

Qy        121       YMDYWGQGTLVIVSS 135
                    | | |||||||||||
Db        121 GNYVRYFFDVWGQGTLVIVSS 140


RESULT 3
US-07-634-278-19
; Sequence 19, Application US/07634278
; Patent No. 5530101
;  GENERAL INFORMATION:
;     APPLICANT:  Queen, Cary L.
;     APPLICANT:  Co, Man Sung
;     APPLICANT:  Schneider, William P.
;     APPLICANT:  Landolfi, Nicholas F.
;     APPLICANT:  Hollingh, Kathleen L.
;     APPLICANT:  Selick, Harold E.
;     TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;     NUMBER OF SEQUENCES:  114
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend Khourie and Crew
;       STREET:  379 Lytton Avenue
;       CITY:  Palo Alto
;       STATE:  California
;       COUNTRY:  US
;       ZIP:  94301
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/634,278
;       FILING DATE:  19-DEC-1990
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/590,274
;       FILING DATE:  28-SEP-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/310,252
;       FILING DATE:  13-FEB-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/290,975
;       FILING DATE:  28-DEC-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William M.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  11823-002600
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 326-2400
;       TELEFAX:  (415) 326-2422
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  135 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-07-634-278-19

  Query Match             75.7%;  Score 545;  DB 1;  Length 135;
  Best Local Similarity   77.8%;  Prod. No. 2.8e-47;
  Matches  105;  Conservative    7;  Mismatches   23;  Indels    0;  Gaps    0;

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Db          1 MGWSWIFLFLLSGTAGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTSYVMHWVRQAP 60

Qy         61 GQGLEWIGVINIYYYDNINYNQKFEGKATMIVDKSISTAYMELSSLRSEDTAVYYCARAAW 120
              |||||||| | | | ||:|||| ;:| |||:|||||||||||||||||||||||  :
Db         61 GQGLEWIGYIYPYNGGTKYNEKFKGRATLTADESTNTAYMELSSLRSEDTAVYYCARGEY 120

Qy        121       YMDYWGQGTLVIVSS 135
                    | | |||||||||||
Db        121 VFDYWGQGTLVTVSS 135
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RESULT 4
US-08-477-728-19
; Sequence 19, Application US/08477728
; Patent No. 5585089
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMMUNOGLOBULIN VARIANTS
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,728
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/934,279
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  135 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-728-19

  Query Match             75.7%;  Score 545;  DB 1;  Length 135;
  Best Local Similarity   77.8%;  Pred. No. 2.8e-47;
  Matches  105;  Conservative    7;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFIDYAIQWVRQAP 60
              ||| | |||   |||||||||||||||||||||||||||||||||| | : ||||||
Db          1 MGWSWIIFLFLLSGTAGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFISYFMHWVRQAP 60

Qy         61 GQGLEWIGVINTYYQNINYNQKFKGKATMTVDKSISTAYMELSSLRSEDTAVYYCARAAW 120
              |||||||| ||     | |||||| ||:|:|:|||||||||||||||||||||||||
Db         61 GQGLEWIGYINPSSGYTEYNQKFKDKATLTADESENTAYMELSSLRSEDTAVYYCARGGG 120

Qy        121 YMDYWGQGILVIVSS 135
                |||||||||||||
Db        121 VFDYWGQGILVIVSS 135


RESULT 5
US-08-474-040-19
; Sequence 19, Application US/08474040
; Patent No. 5693761
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  Co, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  DOYLINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMMUNOGLOBULIN VARIANTS
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,040
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/934,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  135 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-474-040-19

  Query Match             75.7%;  Score 545;  DB 1;  Length 135;
  Best Local Similarity   77.8%;  Pred. No. 2.8e-47;
  Matches  105;  Conservative    7;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFIDYAIQWVRQAP 60
              ||| | |||   |||||||||||||||||||||||||||||||||| | : ||||||
Db          1 MGWSWIIFLFLLSGTAGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFISYFMHWVRQAP 60

Qy         61 GQGLEWIGVINTYYQNINYNQKFKGKATMTVDKSISTAYMELSSLRSEDTAVYYCARAAW 120
              |||||||| ||     | |||||| ||:|:|:|||||||||||||||||||||||||
Db         61 GQGLEWIGYINPSSGYTEYNQKFKDKATLTADESENTAYMELSSLRSEDTAVYYCARGGG 120

Qy        121 YMDYWGQGILVIVSS 135
                |||||||||||||
Db        121 VFDYWGQGILVIVSS 135


RESULT 6
US-08-487-209-19
```

```
; Sequence 19, Application US/08487,203
; Patent No. 5,693,762
;  GENERAL INFORMATION:
;     APPLICANT:  QUEEN, Cary L.
;     APPLICANT:  Co, Man Sung
;     APPLICANT:  SCHNEIDER, William P.
;     APPLICANT:  LANDOLFI, Nicholas F.
;     APPLICANT:  COELINGH, Kathleen L.
;     APPLICANT:  SELICK, Harold E.
;     TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;     NUMBER OF SEQUENCES:  113
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew
;       STREET:  379 Lytton Avenue
;       CITY:  Palo Alto
;       STATE:  California
;       COUNTRY:  US
;       ZIP:  94301
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.[illegible]
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/487,203
;       FILING DATE:  7-JUN-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/634,228
;       FILING DATE:  19-DEC-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/588,274
;       FILING DATE:  26-SEP-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/310,252
;       FILING DATE:  13-FEB-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/290,975
;       FILING DATE:  28-DEC-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William M.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  11923-005P1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 326-2400
;       TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  135 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-487-203C-19

  Query Match             75.7%;  Score 545;  DB 2;  Length 135;
  Best Local Similarity   77.8%;  Pred. No. 2.8e-47;
  Matches  105;  Conservative    7;  Mismatches   23;  Indels    0;  Gaps    0;

Qy           1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAIGWVRQAP 60
               ||: | ||||  |||||||||||||||||||||||||||||||||||| | | ||||||
Db           1 MGWSWIFLFLLSGTAGVHSGVQLVQSGAEVKEPGSSVKVSCKASGYTFTSYYMHWVRQAP 60

Qy          61 GQGLEWIGVINTYYGNINYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
               |||||||| ||     | |||||| |||| |||||||||||||||||||||||||||
Db          61 GQGLEWIGYINPSTGYTEYNQKFKDKATITADESTNTAYMELSSLRSEDTAVYYCARGGG 120

Qy         121 YMDYWGQGTLVTVSS 135
                 ||||||||||||||
Db         121 VFDYWGQGTLVTVSS 135


RESULT 7
US-08-484-537C-19
; Sequence 19, Application US/08484537
; Patent No. 6180370
;  GENERAL INFORMATION:
;     APPLICANT:  QUEEN, Cary L.
;     APPLICANT:  Co, Man Sung
;     APPLICANT:  SCHNEIDER, William P.
;     APPLICANT:  LANDOLFI, Nicholas F.
;     APPLICANT:  COELINGH, Kathleen L.
;     APPLICANT:  SELICK, Harold E.
;     TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;     NUMBER OF SEQUENCES:  113
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend Khourie and Crew
;       STREET:  379 Lytton Avenue
;       CITY:  Palo Alto
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94301
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/303,569B
;       FILING DATE:  07-SEP-1994
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Trujillo, Doreen Yatko
;       REGISTRATION NUMBER:  35,719
;       REFERENCE/DOCKET NUMBER:  CARP 0232
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-3100
;       TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  81:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  135 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-303-569B-81

  Query Match             75.7%;  Score 545;  DB 2;  Length 135;
  Best Local Similarity   77.8%;  Pred. No. 2.8e-47;
  Matches  105;  Conservative    7;  Mismatches   23;  Indels    0;  Gaps    0;

Qy           1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYAIGWVRQAP 60
               ||: | ||||  |||||||||||||||||||||||||||||||||||| | | ||||||
Db           1 MGWSWIFLFLLSGTAGVHSGVQLVQSGAEVKEPGSSVKVSCKASGYTFTSYYMHWVRQAP 60

Qy          61 GQGLEWIGVINTYYGNINYNQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
               |||||||| ||     | |||||| |||| |||||||||||||||||||||||||||
Db          61 GQGLEWIGYINPSTGYTEYNQKFKDKATITADESTNTAYMELSSLRSEDTAVYYCARGGG 120

Qy         121 YMDYWGQGTLVTVSS 135
                 ||||||||||||||
Db         121 VFDYWGQGTLVTVSS 135
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;       STATE:  California
;       COUNTRY:  US
;       ZIP:  94301
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/184,547
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/634,278
;       FILING DATE:  19-DEC-1990
;       APPLICATION NUMBER:  US 07/590,274
;       FILING DATE:  28-SEP-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/310,252
;       FILING DATE:  14-FEB-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/290,975
;       FILING DATE:  28-DEC-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William M
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  11823 002600
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 326-2400
;       TELEFAX:  (415) 326-2422
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  135 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-484-537-19

  Query Match             75.7%;  Score 545;  DB 4;  Length 135;
  Best Local Similarity   77.8%;  Pred. No. 2.8e-47;
  Matches  105;  Conservative    7;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCEASGYTFTDYAIQWVRQAP 60
              ||:| : |||:   |||||||||||||||||||||||||||||||||| | : ||||||
Db          1 MGWSWIFLFLLSGTAGVHSEVQLVESGAEVKKPGESLKISCKGSGYSFMDWVRQMP 57

Qy         61 GQGLEWIGVINIYYGTNTYNQKFEGRATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
              |||||||| ||      | ||||||| |||:| ||||:|||||||||||||||||||||
Db         58 GQGIEWIGYINPSTGYTEYNQKFEDRVTITADESTNTAYME-LSSLRSEDTAVYYCARSY 116

Qy        121 YMDYWGQGTLVTVSS 135
                 |||||||||||||
Db        117 VFDYWGQGTLVTVSS 131


RESULT 9
PCT-US91-02942-5
; Sequence 5, Application PCT/US9102942
;  GENERAL INFORMATION:
;     APPLICANT:  ROTHLEIN, ROBERT
;     APPLICANT:  ADAIR, JOHN R.
;     APPLICANT:  ATHWAL, DILJEET S.
;     TITLE OF INVENTION:  HUMANIZED CDR GRAFTED FCAM 1 ANTIBODY
;     NUMBER OF SEQUENCES:  102
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;       STREET:  1225 Connecticut Ave. NW Suite 300
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US91/02942
;       FILING DATE:  19910429
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9009549.8
;       FILING DATE:  27-APR-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FOX, SAM L.
;       REGISTRATION NUMBER:  30,453
;       REFERENCE/DOCKET NUMBER:  1011.058600
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 466-0800
;       TELEFAX:  (202) 833-8716
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  163 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US91-02942-5

  Query Match             73.8%;  Score 531.5;  DB 5;  Length 163;
  Best Local Similarity   70.4%;  Pred. No. 7.8e-46;
  Matches   92;  Conservative   18;  Mismatches   28;  Indels    5;  Gaps    1;

Qy          1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCEASGYTFTDYAIQWVRQAP 60
              |||:|||||||| |||| :||||| ||| :: :|| |||:||| |||:| |||| ||:::
Db          1 MGWSWIFLFLVAIAIGVHSEVQLVESGGELVKPGGSLRLSCAASGFTFSDYAIHWVKESH 60

Qy         61 GQGLEWIGVINIYYGTNTYNQKFEGRATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
              : |||||||: |  :|||||||||||||||||||:|||:||: | |||:|:|||||  |
Db         61 AEGLEWLVVISTYSGINNYNQEFEDRAIMSVDESSNIAYLQLASLKSEDSAIYYCARQGW 120

Qy        121 YMDYWGQGTLVTVSS 135
                :  |||||||:|||||
Db        121 LISFDYWGQGTLLIVSS 138


RESULT 10
US-08-836-561-63
; Sequence 63, Application US/08836561
; Patent No. 6418032
;  GENERAL INFORMATION:
;     APPLICANT:  KOIKE, Masamichi
;     APPLICANT:  ITOYA, Akiko
;     APPLICANT:  NAKAMURA, Kazuyasu
;     APPLICANT:  IIDA, Akihiro
;     APPLICANT:  ANAZAWA, Hidebaru
;     APPLICANT:  HANAI, No. 6018042no
;     APPLICANT:  TAKAISU, Kiyoshi
;     TITLE OF INVENTION:  Antibody Against Human Interleukin 5
;     TITLE OF INVENTION:  Receptor Alpha Chain
;     NUMBER OF SEQUENCES:  106
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Pennie & Edmonds LLP
;       STREET:  1155 Avenue of the Americas
;       CITY:  New York
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/836,561
;       FILING DATE:  09 MAY-1997
;       CLASSIFICATION:  424
```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 232084/95
; FILING DATE: 11 SEP 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton I
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7889 115 999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790 9090
; TELEFAX: 212 869 9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-830-561-63

Query Match 74.7%; Score 546.5; DB 3; Length 140;
Best Local Similarity 73.6%; Pred. No. 8.6e-46;
Matches 103; Conservative 11; Mismatches 21; Indels 5; Gaps 2;

Qy 1 MGWNCIIFFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIQWVRQAP 60
Db 1 MEWSWIFLFLLSGTAGVHSEVQLVQSGAEVKKPGASVKVSCKASGYIFSSYVIHWVRQAP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFKGKAIMIVDKSISTAYMELSSLRSEDTAVYYCARAA- 119
Db 61 GQGLEWMGYINPYNDGTKYNERFKGRVTIIADESTSTAYMELSSLRSEDTAVYYCAREGI 120

Qy 120 WY MDYWGQGTLVTVSS 135
Db 121 RYYGLIGDYWGQGTLVTVSS 140

RESULT 11
US-07-916-098A-45
; Sequence 45, Application US/07/916,098A
; Patent No. 5871742
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HUMANIZED USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09417
; FILING DATE: No. 5871742ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871742ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gibbons, M. Patrick
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,410-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715 1000
; TELEFAX: (312) 715 1234
; TELEX: 910/221 5317
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-916-098A-45

Query Match 74.6%; Score 540; DB 2; Length 467;
Best Local Similarity 72.5%; Pred. No. 4e-45;
Matches 103; Conservative 11; Mismatches 20; Indels 8; Gaps 2;

Qy 1 MGWNCIIFFLVTIATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIQWVRQAP 60
Db 1 MDWTWRVFCLLAVAPGAHSQVQLQESGAEVKKPGASVKVSCKASGYIFSYVIHWVRQAP 60

Qy 61 GQGLEWIGVINIYYDNINYNQKFKGKAIMIVDKSISTAYMELSSLRSEDTAVYYCAR- 117
Db 61 GQGLEWIGYINPYNDGTDYDEKFKGKATVTSDTSTAYMELSSLRSEDTAVYYCARSD- 120

Qy 118 - -AAWYMDYWGQGTLVTVSS 135
Db 121 NYAIGAWFA YWGQGTLVTVSS 141

RESULT 12
PCT-US93-11611-11
; Sequence 11, Application PC/US9311611
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Landolfi, Nicholas F.
; TITLE OF INVENTION: Humanized Antibodies Reactive with CD18
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11611
; FILING DATE: 30-NOV-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,949
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11622-45
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

RESULT 13
US-08-513-968-44
; Sequence 44, Application US/08513968
; Patent No. 5714143
; GENERAL INFORMATION:
; APPLICANT: EDA, Yasuyaki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: MAKIZUMI, Keiichi
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSAIOMI, Kiyoshi
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,968
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 78913/1993
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EDA 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-513-968-44

Query Match 73.5%; Score 529.5; DB 3; Length 138;
Best Local Similarity 73.9%; Pred. No. 1e-45;
Matches 102; Conservative 14; Mismatches 20; Indels 3; Gaps 1;

Qy 1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIGWVRQAP 60
Db 1 MGWSWIFLFLLSGTAGVHSQVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMNWVRQAP 60

Qy 61 GQGLEWIGWINTYTGEPTYADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCARDYG 120
Db 61 GQGLKWMGWINTNTGNPTYAEEFKGRFAFSFETSASTAYLQISNLKNEDTATYFCARDYG 120

Qy 121 WYFDVWGQGTTVTVSS 136
Db 121 WYFDVWGQGTLVTVSS 136

RESULT 14
US-08-656-586-8
; Sequence 8, Application US/08656586
; Patent No. 5843597
; GENERAL INFORMATION:
; APPLICANT: Iso, J. Yun
; APPLICANT: Cole, Michael S.
; APPLICANT: Anasetti, Claudio
; TITLE OF INVENTION: Mutated No. 58-45-97activating Ig62 Domains and
; TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,586
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11826-007210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-656-586-8

Query Match 73.5%; Score 529; DB 2; Length 139;
Best Local Similarity 74.1%; Pred. No. 1.1e-45;
Matches 103; Conservative 20; Mismatches 22; Indels 4; Gaps 1;

Qy 1 MGWNCIIFFLVATATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYIFTDYAIGWVRQAP 60
Db 1 MGWSWIFLFLLSGTAGVHSQVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMNWVRQAP 60

Qy 61 GQGLEWIGWINTYTGEPTYADDFKGRFAFSLETSASTAYLQINNLKNEDMATYFCARDYG 120
Db 61 GQGLEWMGWINTNTGNPTYAEEFKGRFAFSFETSASTAYLQISNLKNEDTATYFCARDYG 120

Qy 121 WYFDVWGQGTLVTVSS 136
Db 121 WYFDVWGQGTLVTVSS 136

RESULT 15

```
US-08-147-011B-102
; Sequence 102, Application US/08/147,011B
; Patent No. 5795965
;  GENERAL INFORMATION:
;    APPLICANT:  ISHIOKA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN 6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/147,011B
;      FILING DATE:  20-DEC-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  5451-2/3/AA-k
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  102:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  135 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-147-011B-102

  Query Match              75.2%;  Score 527;  DB 1;  Length 135;
  Best Local Similarity    75.6%;  Pred. No. 1.7e-45;
  Matches  102;  Conservative    8;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MGWNCIIFFLVIIATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAP 60
              | |   :| |:  | | ||||||||||||||||||:|||||||||||:|| | | ||||||
Db          1 MDWIWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGYSFISYYIHWVRQAP 60

Qy         61 GQGLEWIGVINTYYGNTNYNQKFKGRATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAW 120
              |||:| || |: :   ||||||||| |||| ||:||.|:|||||||||||||||||||||
Db         61 GQGLEWMGYIDPENGGTSYNQKFKGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGGN 120

Qy        121 YMDYWGQGTLVTVSS 135
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Db        121 FFAYWGQGTLVTVSS 135


Search completed: June 24, 2003, 15:14:08
Job time : 20.6666 secs
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QM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 13:02:05 ; Search time 1844.72 Seconds
(without alignments)
27729.748 Million cell updates/sec

Title: US-09-249-011b-7
Perfect score: 966
Sequence: 1 atgaattcacaatgccaagtt.....aggatccaagcttctagataaaa 966

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2654640 seqs, 1455140278 residues

Total number of hits satisfying chosen parameters: 5309280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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14: gb_vi:*
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17: em_hum:*
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27: em_sts:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	966	100.0	462	10	MUSIGKPALI	M28833 Mus musculu
2	942	85.9	490	6	AJ12233	AJ12233 variable to
3	836.2	84.9	436	10	MMU25858	U25858 Mus musculus
4	834.6	84.2	419	10	MMU97070	U97070 Mus musculu
5	832	83.8	948	6	A44968	A44968 Sequence 24
6	832	83.8	948	6	I64459	I64459 Sequence 24
7	801.4	76.1	401	10	MMLA21LEV	X65774 M.musculus
8	798.2	75.8	402	10	MUSIGKALA	M98042 Mouse Ig ke
9	796.6	74.9	479	10	AB050076	AB050076 Mus muscu
10	796	74.7	336	10	AF163745	AF163745 Mus muscu
11	796	74.7	336	10	MD1GKVAR	Z22055 M.domestic
12	796	74.7	389	10	AB028876	AB028876 Mus muscu
13	795.2	74.5	408	10	S87289	S87289 IgM kappa
14	795	74.5	389	10	MUSIGKV19	L19439 Mus musculu
15	794.4	74.3	336	10	AF321954	AF321954 Mus muscu
16	792.8	74.2	336	10	MD1G3VA1	Z22030 M.domestic
17	792.8	74.2	336	10	MD1GKVA0	Z22030 M.domestic
18	791.4	74.1	388	10	AF321942	AF321942 Mus muscu
19	788.6	73.8	399	6	A47511	A47511 Sequence 3
20	788.6	73.8	399	6	A80111	A80111 Sequence 3
21	786.4	73.6	336	10	MMJ22647	AJ22647 mouse DNA
22	786.4	73.6	337	10	S74056	S74056 Ig V62 ligh
23	785.4	73.5	385	10	AF321956	AF321956 Mus muscu
24	785.4	73.5	389	6	AF2521	AF2521 Sequence 40
25	785.4	73.5	460	6	AF62617	AF62617 Sequence 30
26	784.8	73.9	336	10	MUSIGKAIB	M97052 Mouse Ig ke
27	784.8	73.9	336	10	MUSIGKALV	M97929 Mouse Ig ke
28	784.8	73.9	336	10	MM1KACIV	Z21454 M.musculus
29	784.8	73.9	389	10	MMU60464	U60464 Mus musculu
30	784.4	73.8	336	10	MMU55647	U55647 Mus musculu
31	784.2	73.8	336	10	MMU55674	U55674 Mus musculu
32	784.2	73.8	336	10	MD1GKVAG	Z22040 M.domestic
33	783.2	73.8	342	6	AR135063	AR135063 Sequence
34	783.0	73.7	336	10	AF321944	AF321944 Mus muscu
35	781.8	73.7	764	10	MMY15982	Y15982 Mus musculu
36	781.6	73.7	339	10	MMF343768	AJ343768 Mus muscu
37	781.6	73.7	600	10	AF349145	AF349145 Mus muscu
38	781.4	73.7	336	10	MMU55674	U55674 Mus musculu
39	780.6	73.6	399	10	MMIGHA	M99524 M.musculus
40	779.8	73.7	411	10	MMIGGVJ5	X02101 M.musculus
41	779.8	73.7	1443	6	AR063210	AR063210 Sequence
42	779	73.5	427	6	A94042	A94042 Sequence 28
43	779	73.5	427	6	AX011127	AX011127 Sequence
44	779	73.5	463	6	AR109948	AR109948 Sequence
45	779	73.5	8068	6	A94046	A94046 Sequence 32

ALIGNMENTS

RESULT 1
MUSIGKPALI
LOCUS MUSIGKPALI 462 bp mRNA linear 30-JUN-2004
DEFINITION Mus musculus IgK chain (anti-Pseudomonas aeruginosa lipoprotein 1 antibody) mRNA, 5' end.
ACCESSION M28833
VERSION M28833.1 GI:576509
KEYWORDS V segment; anti-lipoprotein antibody; immunoglobulin kappa chain; immunoglobulin light chain.
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) hybridoma cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 462)

```
  AUTHORS   Margolies,M., Bokhari,F.A., Blazo,W., Yanagihara,D.L., Lachenauer,M. and
            Bondelid,R.
  TITLE     Cloning and characterization of cDNAs coding for the heavy and
            light chains of a monoclonal antibody specific for Pseudomonas
            aeruginosa outer membrane protein I
  JOURNAL   Gene 74 (2), 335-345 (1988)
  MEDLINE   89025225
   PUBMED   3149044
COMMENT     On Nov 28, 1994 this sequence version replaced gi:341017.
FEATURES             Location/Qualifiers
     source          1..462
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /db_xref="taxon:10090"
                     /cell_line="MAB 7A1"
                     /tissue_type="hybridoma"
     gene            1..462
                     /gene="lgk"
     CDS             16..462
                     /gene="lgk"
                     /codon_start=1
                     /product="immunoglobulin kappa chain"
                     /protein_id="AAA53292.1"
                     /db_xref="GI:341018"
                     /translation="METDTLLLWVLLLWVPGSTGDIVMSQSPSSLAVSAGEKVTMSC
                     KSSQSLLNSGNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFIGSGSGTDFTLTIS
                     SVQAEDLAVYYCQQYYNYPLTFGSGTKLEIKRADAAPTVSIFPPSSE"
     sig_peptide     1..48
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                     /product="immunoglobulin kappa chain"
BASE COUNT      114 a    116 c    121 g    111 t
ORIGIN

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  Best Local Similarity   91.2%;  Pred. No. 7e-104;
  Matches  361;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 ATGGAGACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGCTCCACCGGCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGGAGACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGCTCCACCGGCG 75

Qy         61 ACATCGTGATGTCTCAGTCTCCATCCTCCCTGTCTGTGTCAGCAGGAGAGAAGGTCACTAT 120
              |||||||||| || |||||||||||   ||||||||||      ||| | ||| || ||||
Db         76 ACATCCAGTTGACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCAT 135

Qy        121 AACCTGCAGTCCAGTCAGAGCCTTTTAAACAGTGGAAATCAAAAGAACTACTTGGCCTGGT 180
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 ACCTGCAGTCCAGTCAGAGCCTTTTAAACAGTGGAAATCAAAAGAACTACTTGGCCTGGT 195

Qy*       181 TCCAGCAGAAACCAGGGCAGCCTCCTAAAGCTGCTGATCTACTGGGCATCCACTAGGGAA 240
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        196 TCCAGCAGAAACCAGGGCAGCCTCCTAAAGCTGCTGATCTACTGGGCATCCACTAGGGAA 255

Qy        241 TCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 TCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC 315

Qy        301 AGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAATTATCCT 360
              ||||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        316 AGCAGTGAGGTCCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAATTATCCT 375

Qy        361 TACACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 396
              |||||||| || ||||||| |||||||||||||||
Db        376 TACACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 411

RESULT 2
AI43733
LOCUS       AI43733                 480 bp    DNA     linear   PAT 03-JAN-1994
DEFINITION  variable region of a monoclonal antibody which cross reacts with 19
            known Pseudomonas serotypes.
ACCESSION   AI43733
VERSION     AI43733.1  GI:491741
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Bondelid,R., Margolies,M. and von Specht,B.U.
  TITLE     Monoclonal antibodies to Pseudomonas aeruginosa, their production
            and use
  JOURNAL   Patent: EP 0338395-A 1 25-OCT-1989;
            BEHRINGWERKE Aktiengesellschaft
FEATURES             Location/Qualifiers
     source          1..480
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     CDS             37..>480
                     /codon_start=1
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                     /product="V region of a monoclonal antibody, cross reacts
                     with 19 P.aeruginosa serotypes"
                     /protein_id="AAA01126.1"
                     /db_xref="GI:491742"
                     /translation="MESQAQVLILLWVSGTCGDIVMSQSPSSLAVSAGEKVTMSC
                     KSSQSLLNSGNQKNFLAWYQQKPGQPPKLLIYWASTRESGVPDRFIGSGSGTDFTLTIS
                     SVQAEDLAVYYCQQYYNYPLTFGSGTKLEIKRADAAPTVSIFPPSSE"
BASE COUNT      115 a    117 c    136 g    112 t
ORIGIN

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  Best Local Similarity   91.2%;  Pred. No. 7e-104;
  Matches  361;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 ATGGAGACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGCTCCACCGGCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         37 ATGGAGACCGACACCCTGCTGCTGTGGGTGCTGCTGCTGTGGGTGCCAGGCTCCACCGGCG 96

Qy         61 GACATCGTGATGTCTCAGTCTCCATCCTCCCTGTCTGTGTCAGCAGGAGAGAAGGTCACTAT 120
              |||||||||| || |||||||||||   ||||||||||      ||| | ||| || ||||
Db         97 GACATCCAGTTGACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCAT 156

Qy        121 AACCTGCAGTCCAGTCAGAGCCTTTTAAACAGTGGAAATCAAAAGAACTACTTGGCCTGGT 180
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 ACCTGCAGTCCAGTCAGAGCCTTTTAAACAGTGGAAATCAAAAGAACTACTTGGCCTGGT 216

Qy*       181 TCCAGCAGAAACCAGGGCAGCCTCCTAAAGCTGCTGATCTACTGGGCATCCACTAGGGAA 240
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        217 TCCAGCAGAAACCAGGGCAGCCTCCTAAAGCTGCTGATCTACTGGGCATCCACTAGGGAA 276

Qy        241 TCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 AGTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC 336

Qy        301 AGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAATTATCCT 360
              ||||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        337 AGCAGTGAGGTCCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAATTATCCT 396

Qy        361 TACACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 396
              |||||||| || ||||||| |||||||||||||||
Db        397 TACACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 432

RESULT 3
MMU62050
LOCUS       MMU62050                480 bp    mRNA    linear   ROD 15-SEP-1993
DEFINITION  Mus musculus polyreactive autoantibody, immunoglobulin light chain
            kappa mRNA, partial cds.
ACCESSION   U62050
VERSION     U62050.1  GI:1438580
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 406)
  AUTHORS   Draw,I., Maynac,C., Pritsch,O., Buckle,M., Alzari,P.M. and
            Dighiero,G.
  TITLE     Structural and affinity studies of IgM polyreactive natural
            autoantibodies
  JOURNAL   J. Immunol. 158 (2), 968-976 (1997)
  MEDLINE   97140971
   PUBMED   8993018
REFERENCE   2  (bases 1 to 406)
  AUTHORS   Draw,I., Maynac,C., Pritsch,O., Buckle,M., Alzari,P.M. and
            Dighiero,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-1996) Laboratoire d'Immunohematologie et
            d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris
            75724 Paris Cedex 15, France
FEATURES             Location/Qualifiers
     source          1..406
                     /organism="Mus musculus"
                     /strain="[illegible]"
                     /db_xref="taxon:10090"
                     /sex="[illegible]"
                     /note="hybridoma M2[illegible] cell [illegible] fused with
                     SP2/0 myeloma cells"
     CDS             <1..>406
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                     /protein_id="AAB47613.1"
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                     /translation="[illegible]
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BASE COUNT      101 a     99 c     108 g     98 t
ORIGIN

  Query Match          84.7%;  Score 336.2;  DB 1;  Length 406;
  Best Local Similarity   92.7%;  Pred. No. 1.4e-102;
  Matches  358;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

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Db          1 ATGGATTTCACAGGCCAGGTTCTTATATTGCTGCTGCTATGGTATCTGGTACTCCTGGG 60

Qy         61 GACATTGTGCTGACACAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACATTGTGCTGACACAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACA 120

Qy        121 ATCTCCTGCAGAGCCAGTGAAAGTGTTGAATATTATGTCACTAGTTTAATGCAGTGGTAC 180
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Qy        181 CAGCAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAACGTAGAAGAT 240
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Qy        241 GCTGCAACATATTACTGTCAGCAAAGTAATGAGGATCCGTACACGTTCGGAGGGGGGACC 300
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Qy        301 AAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 GAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAA 420
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Db        361 GAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAA 420

Qy        421 GACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGT 480

Qy        481 TGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACC 540

Qy        541 AAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT 600

Qy        601 CCCATTGTCAAGAGCTTCAACAGGAATGAGTGT 633
              |||||||||||||||||||||||||||||||||
Db        601 CCCATTGTCAAGAGCTTCAACAGGAATGAGTGT 633


RESULT 4
MMU07570
LOCUS       MMU07570                 419 bp    mRNA    linear   ROD 11-JUN-1997
DEFINITION  Mus musculus immunoglobulin light chain variable region (IgK) mRNA,
            partial cds.
ACCESSION   U07570
VERSION     U07570.1  GI:2183076
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Foljo,G.C.S., Sabbada,L., Carneiro,C.R.W. and Brigido,M.M.
  TITLE     Variable region structure and Staphylococcal protein A binding
            specificity of a mouse anti laminin receptor monoclonal IgM
  JOURNAL   Immunology (1997) In press
REFERENCE   2  (bases 1 to 419)
  AUTHORS   Brigido,M.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Biologia Celular, Universidade de Brasilia,
            Campus Universitario, Asa Norte, Brasilia, DF 70910-900, Brazil
FEATURES             Location/Qualifiers
     source          1..419
                     /organism="Mus musculus"
                     /strain="Balb/c"
                     /db_xref="taxon:10090"
                     /cell_line="1B12"
                     /cell_type="hybridoma"
     gene            1..419
                     /gene="IgK"
     CDS             21..419
                     /gene="IgK"
                     /note="rearranged VK1 to JK1 region"
                     /codon_start=1
                     /function="[illegible] variable region"
                     /protein_id="AAB60896.1"
                     /db_xref="GI:2183077"
                     /translation="MDSQAQVLILLLWVSGTCGDIVMSQSPSSLAVSAGEKVTMSCK
                     SSQSLLESRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTI
                     SVQAEDLAIYYCKQSYNLYTFGGGTKLEIKR"
BASE COUNT      105 a     101 c     115 g      98 t
ORIGIN

  Query Match          84.2%;  Score 333.6;  DB 1;  Length 419;
  Best Local Similarity   90.2%;  Pred. No. 1e-101;
  Matches  357;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy          1 ATGGATTTCACAGGCCAGGTTCTTATATTGCTGCTGCTATGGTATCTGGTACTCCTGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ATGGATTTCACAGGCCAGGTTCTTATATTGCTGCTGCTATGGTATCTGGTACTCCTGGG 80

Qy         61 GACATTGTGCTGACACAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GACATTGTGCTGACACAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACA 140

Qy        121 ATCTCCTGCAGAGCCAGTGAAAGTGTTGAATATTATGTCACTAGTTTAATGCAGTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ATCTCCTGCAGAGCCAGTGAAAGTGTTGAATATTATGTCACTAGTTTAATGCAGTGGTAC 200

Qy        181 CAGCAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAACGTAGAAGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 CAGCAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAACGTAGAAGAT 260

Qy        241 GCTGCAACATATTACTGTCAGCAAAGTAATGAGGATCCGTACACGTTCGGAGGGGGGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 GCTGCAACATATTACTGTCAGCAAAGTAATGAGGATCCGTACACGTTCGGAGGGGGGACC 320

Qy        301 AAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGT 380

Qy        361 GAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAA 440
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RESULT 6
A41668
LOCUS       A41668                   940 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 24 from Patent WO9515382.
ACCESSION   A41668
VERSION     A41668.1  GI:1182554
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 940)
  AUTHORS   Rose,M.S., Boot,C., Copley,C.J., Paterson,D.S., Bell,S.M.,
            Wright,A.F. and Blakey,D.C.
  TITLE     IONISING RADIATION DIRECTED ANTIBODY THERAPY ANTIGEN
  JOURNAL   Patent: WO 9515382-A 24-JUN-1995;
            ZENECA LTD (GB)
COMMENT     other publication GB 2287771 19950927
            other publication CA 2174972 19950608
            other publication ZA 9409266 19950705
            other publication AU 1114095 19950620.
FEATURES             Location/Qualifiers
     source          1..940
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      241 a    266 c    213 g    220 t
ORIGIN

  Query Match             83.8%;  Score 332;  DB 6;  Length 940;
  Best Local Similarity   89.9%;  Prod. No. 3.8e-101;
  Matches  356;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy          1 ATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        10 ATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCATGGGTATCTGGAACCTGTGGG 69

Qy         61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTGTCTCTAGGGGAGAGGGCCACT 120
              |||||||||| || ||||||||||    |||||||||         |||||||| || |||
Db         70 GACATTGTGATGTCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACC 129

Qy        121 ATTAACTGCAAATCCAGTCAGAGTCTGTTAACAGTAGAAACCCGAGAGAACTACTTGGCT 180
              || |||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        130 ATGAGCTGCAAATCCAGTCAGAGTCTGTTAACAGTAGAAACCCGAGAGAACTACTTGGCT 189

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              |||||||||| |||||||||| |||||||||||||||||||||||||||||||||||||
Db        190 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 249

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        250 ACATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 309

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGGCAATCTTATAATCTT 360
              ||||||||| |||||||||||||| |||| ||||||||||| ||||||||||| |||| 
Db        310 ATCAGCAGTCTGCAGGCTGAAGACGTTGGTGTTTATTACTGCAATCAATCTTATAATCCT 369

Qy        361 TACACGTTCGGAGCAGGGACCAAGCTGGAAATAAAA 396
                |||||||    || |||||| ||||||| |||
Db        370 CCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 405


RESULT 7
MMLA2LEV
LOCUS       MMLA2LEV                 402 bp    mRNA    linear   ROD 17-JUN-1998
DEFINITION  M.musculus DNA for IgE antibody light chain (VJ).
ACCESSION   X65774
VERSION     X65774.1  GI:312076
KEYWORDS    IgE antibody; J segment; light chain; V region.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Keller,H., Schneeg,I., Geley,S., Helmberg,A., Varga,J.M. and
            Keller,E.
  TITLE     Mechanism of allergic cross reactions: III. cDNA cloning and
            variable-region sequence analysis of two IgE antibodies specific
            for trinitrophenyl
  JOURNAL   Mol. Immunol. 29 (2), 161-166 (1992)
  MEDLINE   92178225
   PUBMED   1541229
FEATURES             Location/Qualifiers
     source          1..402
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /cell_line="SGE.a2 (ATCC 118142)"
     CDS             1..402
                     /codon_start=1
                     /product="IgE antibody light chain (VJ)"
                     /protein_id="CAA46658.1"
                     /db_xref="GI:312077"
                     /translation="MDSQAQVLMLLLLWVSGTCGDIVMSQSPSSLAVSVGEKVTMSCK
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                    SSQSLLYSSNQKNYLAWYQRKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS
                    SVKAEDLAVYYCQHYYSSPYTFGGGTKLEIK"
     sig_peptide    1..57
     V_region       1..401
                    /product "IgE antibody light chain (VJ)"
     J_segment      366..401
BASE COUNT      117 a     91 c     105 g     103 t
ORIGIN

  Query Match          74.5%;  Score 298.2;  DB 10;  Length 402;
  Best Local Similarity   86.5%;  Pred. No. 8.7e-91;
  Matches  445;  Conservative    0;  Mismatches   51;  Indels    3;  Gaps    1;

Qy          1 ATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGTTATCTGGCACCTGTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATGGATTCACAGGCCCAGGTTCTTATGTTACTGCTGCTATGGTTATCTGGTACCTGTGGGG 62

Qy         61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTGTCTGCTGGAGAGAGGGCCACT 120
              |||||||||| |||||||||||    ||||| |||||     | |||||||| ||  |||
Db         63 GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTTACT 122

Qy        121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGGAGAGAACTACTTGGCT 180
              || |||||| ||||||||||| || |  | |||| |  | | ||||||||||||
Db        123 ATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTAGCAATCAAAAGAACTACTTGGCC 182

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              ||||||||| |||||||||||| |||||||||||||||| ||||||||||||||||||||
Db        183 TGGTACCAGCAGCAAACCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCATCCACTAGG 242

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
              |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||
Db        243 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 302

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAATCTTATA---AT 357
              |||||||| || |||||||||| ||||||||||||||||   ||| | ||||    |
Db        303 ATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTCT 362

Qy        358 CTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
              | | |||||||||||  ||||||||| ||||||||||
Db        363 GCTCACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 401


RESULT 8
M98012
LOCUS       M98012                  402 bp    mRNA    linear   ROD 14-JAN-1993
DEFINITION  Mouse Ig rearranged K-chain mRNA V-region, 5' end.
ACCESSION   M98012
VERSION     M98012.1  GI:196749
KEYWORDS    V-region; hepatitis; immunoglobulin light chain; processed gene.
SOURCE      Mus musculus (strain BALB/c, sub-species domesticus) spleen cDNA to
            mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Hong,H.J., Kim,A.K., Kyu,C.I., Park,S.S., Chung,B.S., Kwon,K.S.,
            Kim,K.L., Kim,J. and Ban,M.H.
  TITLE     Cloning and characterization of cDNAs coding for heavy and light
            chains of a monoclonal antibody specific for pre-S2 antigen of
            hepatitis B virus
  JOURNAL   Gene 121 (2), 331-335 (1992)
  MEDLINE   93077049
   PUBMED   1446862
FEATURES             Location/Qualifiers
     source          1..402
                     /organism "Mus musculus"
                     /strain "BALB/c"
                     /sub_species "domesticus"
                     /db_xref "taxon:10090"
                     /map "Chromosome 6"
                     /cell_line "H8"
                     /cell_type "hybridoma"
                     /tissue_type "spleen"
     CDS             1..402
                     /partial
                     /function "specific for pre-S2 antigen of hepatitis B
                     virus"
                     /codon_start=1
                     /product "immunoglobulin kappa-chain"
                     /protein_id "AAA88777.1"
                     /db_xref "GI:196750"
                     /translation "MDSQAQVLMLLLLWVSGTCGNIVMSQSPSSLAVSVGEKVTMSCK
                     SSQSLLYSSNQKNYLAWYQRKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS
                     SVKAEDLAVYYCQHYYSSPYTFGGGTKLEIKR"
     sig_peptide     1..60
     mat_peptide     61..402
                     /partial
                     /product "unnamed"
BASE COUNT      102 a     93 c     109 g     107 t
ORIGIN

  Query Match          75.3%;  Score 298.2;  DB 10;  Length 402;
  Best Local Similarity   86.0%;  Pred. No. 1.1e-89;
  Matches  344;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy          1 ATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGTTATCTGGCACCTGTGGGG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATTCACAGGCCCAGGTTCTTATGTTACTGCTGCTATGGTTATCTGGTACCTGTGGGG 60

Qy         61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTGTCTGCTGGAGAGAGGGCCACT 120
              |||||||||| |||||||||||    ||||| |||||     | |||||||| ||  |||
Db         61 GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTTACT 120

Qy        121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGGAGAGAACTACTTGGCT 180
              || |||||| ||||||||||| || |  | |||| |  | | ||||||||||||
Db        121 ATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTAGCAATCAAAAGAACTACTTGGCC 180

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              ||||||||| |||||||||||| |||||||||||||||| ||||||||||||||||||||
Db        181 TGGTACCAGCAGCAAACCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCATCCACTAGG 240

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
              |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||
Db        241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAATCTTATA---AT 357
              |||||||| || |||||||||| ||||||||||||||||   ||| | ||||    |
Db        301 ATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTCT 360

Qy        358 CTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
              | | |||||||||||  ||||||||| ||||||||||
Db        361 GCTCACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 399


RESULT 9
AB050076
LOCUS       AB050076                479 bp    mRNA    linear   ROD 02-APR-2002
DEFINITION  Mus musculus VL0B5 mRNA for anti-dsRNA (REV-RNA) antibody, partial
            cds.
ACCESSION   AB050076
VERSION     AB050076.1  GI:19909927
KEYWORDS    .
SOURCE      Mus musculus (strain:BALB/c) cell_line:hybridoma 9B5 cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Kitagawa,Y., Matsumoto,I., Okubara,E. and Shikata,K.
  TITLE     Immunogenicity of rice dwarf virus ribonucleic acid
  JOURNAL   J. S. C. J. Exp. Med. 122 (3), [illegible] (2001)
  MEDLINE   78034786
   PUBMED   9230770
REFERENCE   2
  AUTHORS   Kitagawa,Y.
  TITLE     anti-dsRNA (REV-RNA) Ab VL region, VL9B5
  JOURNAL   Published only in database (2002)
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REFERENCE   3  (bases 1 to 479)
  AUTHORS   Kitagawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural
            University, Biotechnology Institute, Minami 2-2, Ogata, Akita
            010-0444, Japan (E-mail:kitagawa@ani.akita-pu.ac.jp,
            URL:www.akita-pu.ac.jp/, Tel:+81 185 45 2020(ex.400),
            Fax:+81 185 45 2678)
FEATURES             Location/Qualifiers
     source          1..479
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /db_xref="taxon:10090"
                     /cell_line="hybridoma 9D5"
     gene            1..479
                     /gene="V19D5"
     CDS             26..478
                     /gene="V19D5"
                     /codon_start=1
                     /product="anti dsRNA (RDV RNA) antibody"
                     /protein_id="BAB87168.1"
                     /db_xref="GI:19909928"
                     /translation="MEWSWVFLFFLSVTTGVHSEVQLQQSGPELVKPGASVKISCKA
                     SGQSLLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS
                     SVEAEDLAVYYCQQYYSYPWTFGGGTKLEIKRAAAIVSYEEQTP"
BASE COUNT       127 a       113 c       125 g       124 t
ORIGIN

  Query Match             74.9%;  Score 296.6;  DB 10;  Length 479;
  Best Local Similarity   85.7%;  Pred. No. 3.8e-89;
  Matches  342;  Conservative    0;  Mismatches   54;  Indels    3;  Gaps    1;

Qy          1 ATGGATTTACAGGGCCAGGTTCTTATATTGCTTCTTCTGATCTCTGCTTCTGTGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 ATGGATTTACAGGGCCAGGTTCTTATATTGCTTCTTCTGATCTCTGCTTCTGTGGG 85

Qy         61 GACATTGTGCTGACACAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACT 120
              |||||||||| || |||||||||||    ||||| |||||      | |||||| ||  |||
Db         86 GACATTTTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTTACT 145

Qy        121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAAACTACTTGGCT 180
              || ||||.|| ||||||||||| ||  | | ||||| |  | || ||||||||||||||
Db        146 ATGAGCTGCAAGTCCAGTCAGAGTTTTATATAGCAACAATAAAAGAACTACTTGGC 205

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 TGGTATCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATTTACTGGGCATCCACTAGG 265

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
              |||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        266 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 325

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAA-- AT 357
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||  ||
Db        326 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATTAT 385

Qy        358 TTTACACTTCGGCACAGGGACCAAGCTGGAAATAAAA 394
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Db        386 TCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 424


RESULT 10
AF063475
ID  AF063475                 486 bp    mRNA    linear   ROD 29-JUL-2001
XX
AC   AF063475
XX
DE   Mus musculus mAb 27.4.1 immunoglobulin light chain variable region
     mRNA, partial cds.
XX
AC   AF063475
XX
SV   AF063475.1  GI:5060206
XX
KW
XX
OS   Mus musculus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE   1  (bases 1 to 336)
  AUTHORS   Morrison,N.M., Calvin,J.E., Adderson,E.E. and Cunningham,M.W.
  TITLE     Molecular analysis of cross reactive anti myosin/anti streptococcal
            mouse monoclonal antibodies
  JOURNAL   Mol. Immunol. 37 (15), 901-913 (2000)
  MEDLINE   21176651
   PUBMED   11282394
REFERENCE   2  (bases 1 to 336)
  AUTHORS   Morrison,N.M. and Cunningham,M.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma
            University Health Sciences Center, 940 St. Young Blvd, Oklahoma
            City, OK 73190, USA
FEATURES             location/qualifiers
     source          1..336
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                     /strain="BALB/c"
                     /db_xref="taxon:10090"
                     /note="mAb 27.4.1"
     CDS             <1..>336
                     /note="V-J segments"
                     /codon_start=1
                     /product="immunoglobulin light chain variable region"
                     /protein_id="AAB47024.1"
                     /db_xref="GI:559297"
                     /translation="QIVMSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQ
                     KPGQSPKLLIYWASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLYT
                     FGGGTKLEIK"
BASE COUNT        91 a        83 c        86 g        76 t
ORIGIN

  Query Match             74.7%;  Score 296;  DB 10;  Length 336;
  Best Local Similarity   92.6%;  Pred. No. 5.9e-89;
  Matches  311;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy         61 GACATTGTGCTGACAGTCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACT 120
              |||||||| || |||||||||||    ||||| |||||      | |||||| ||  |||
Db          1 GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTTACT 60

Qy        121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAAACTACTTGGCT 180
              || |||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db         61 ATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAAACTACTTGGCT 120

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 180

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
              |||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATCCT 360
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATCCG 300

Qy        361 TACACGTTCGGAGGGGGCACCAAGCTGGAAATAAAA 396
              |||||||||| ||||||||| ||||||||||||||||
Db        301 TACACGTTCGGAGGGGGCACCAAGCTGGAAATAAAA 336


RESULT 11
MDIGKVAR
ID  MDIGKVAR                 336 bp    mRNA    linear   ROD 05-NOV-1994
DE   Mus musculus immunoglobulin kappa variable region.
AC   X22965
VERSION   X22965.1  GI:297629
KEYWORDS    anti DNA antibody; IgK gene; IgK variable region; immunoglobulin.
SOURCE      Mus musculus domesticus.
  ORGANISM  Mus musculus domesticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 336)
  AUTHORS   Tillman,F.M., Jou,N.T., Hill,R.J. and Marion,T.N.
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  TITLE     Both IgM and IgG anti-DNA antibodies are the products of clonally
            selective B cell stimulation in (NZB x NZW)F1 mice
  JOURNAL   J. Exp. Med. 176 (6), 761-779 (1992)
  MEDLINE   92369414
   PUBMED   1512734
REFERENCE   2  (bases 1 to 336)
  AUTHORS   Marion,T.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAR-1993) Tony N. Marion, Microbiology and
            Immunology, University of, Tennessee, Memphis, 858 Madison Avenue,
            Memphis, TN, 38163, USA
FEATURES             Location/Qualifiers
     source          1..336
                     /organism="Mus musculus domesticus"
                     /strain="(NZB x NZW)F1"
                     /isolate="mouse #1c5"
                     /db_xref="taxon:10092"
                     /chromosome="X"
                     /sex="female"
                     /cell_line="145.4S"
                     /cell_type="hybridoma"
                     /tissue_type="spleen"
                     /dev_stage="somatic variant"
     gene            1..336
                     /gene="IgK"
     CDS             <1..>336
                     /gene="IgK"
                     /function="Kappa light chain variable region typ; anti DNA
                     antibody; Vk8 family"
                     /codon_start=1
                     /product="immunoglobulin variable region"
                     /protein_id="CAA80037.1"
                     /db_xref="GI:297650"
                     /translation="[illegible]
                     KPVQSPPELIYWASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLAVYYCQQYYSYPLTF
                     GGGTKLEIK"
BASE COUNT       91 a     83 c     86 g     76 t
ORIGIN

  Query Match             74.7%;  Score 296;  DB 53;  Length 336;
  Best Local Similarity   92.6%;  Pred. No. 5.2e-80;
  Matches  311;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          61 GACATTGTGATGTCACAGTCTCCAGATTCCCTGGCTGTGTCTCTAGGAGAGAGGGCCACT 120
               ||||||||| || |||||||||| |||||||||| |||||| || |||
Db           1 GACATTGTGATGTCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACT 60

Qy         121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAAACCCGAAGAACTACTTGGCT 180
               || |||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          61 ATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAAACCGAAAGAACTACTTGGCT 120

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
               ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         121 TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 300

Qy         361 TACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 396
               |||||||||||| ||||||||| ||||||||||
Db         301 TACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 336


RESULT 12
AB028876
LOCUS       AB028876                 339 bp    mRNA    linear   ROD 27-MAR-2002
DEFINITION  Mus musculus mRNA for 5.2 IgG light chain (variable region),
            partial cds.
ACCESSION   AB028876
VERSION     AB028876.1  GI:5103290
KEYWORDS    5.2 IgG light chain variable region.
SOURCE      Mus musculus cell line:hybridoma 5.2 cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Yoshida,S., Matsumoka,H., Ino,E., Iwai,K., Arai,M., Sinden,R.E. and
            Ishii,A.
  TITLE     A single-chain antibody fragment specific for the Plasmodium
            berghei ookinete protein Pbs21 confers transmission blockade in the
            mosquito midgut
  JOURNAL   Mol. Biochem. Parasitol. 104 (2), 195-204 (1999)
  MEDLINE   20058748
REFERENCE   2  (bases 1 to 339)
  AUTHORS   Yoshida,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUN-1999) Shigeto Yoshida, Jichi Medical School,
            Department of Medical Zoology, Yakushiji 3311-1,
            Minamikawachimachi, Tochigi 329-0498, Japan
            (E-mail:shineto@jichi.ac.jp, Tel:81 285 58 7339,
            Fax:81 285 44 0489)
FEATURES             Location/Qualifiers
     source          1..339
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /cell_line="hybridoma 5.2"
     gene            1..339
                     /gene="5.2 VL"
     CDS             <1..>339
                     /gene="5.2 VL"
                     /note="Light chain variable region of 5.2 monoclonal
                     antibody"
                     /codon_start=1
                     /product="5.2 IgG light chain"
                     /protein_id="BAA78004.1"
                     /db_xref="GI:5103291"
                     /db_xref="UNIPROT:AB028876"
                     /translation="[illegible]
                     KPVQSPPELIYWASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLAVYYCQQYYSYPLTF
                     GGGTKLEIKQ"
BASE COUNT       92 a     84 c     87 g     76 t
ORIGIN

  Query Match             74.7%;  Score 296;  DB 10;  Length 339;
  Best Local Similarity   92.6%;  Pred. No. 5.2e-80;
  Matches  311;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          61 GACATTGTGATGTCACAGTCTCCAGATTCCCTGGCTGTGTCTCTAGGAGAGAGGGCCACT 120
               ||||||||| || |||||||||| |||||| || |||
Db           1 GACATTGTGATGTCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACT 60

Qy         121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAAACCCGAAGAACTACTTGGCT 180
               || |||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          61 ATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAAACCGAAAGAACTACTTGGCT 120

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
               ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         121 TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 300

Qy         361 TACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 396
               |||||||||||| ||||||||| ||||||||||
Db         301 TACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 336
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RESULT 13
2M1200
LOCUS       2M1200                  408 bp    mRNA    linear   ROD 27-MAY-1995
DEFINITION  IgM Kappa chain variable region gene 1 from BALB/c anti-(NP)
            HAP I hybridoma cells, mRNA Partial, 408 nt.
ACCESSION   2M1200
VERSION     2M1200.1  GI:1294409
KEYWORDS    .
SOURCE      Balb/c sp. IgM HAP I hybridoma cells.
  ORGANISM  Balb/c sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Balb/c.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Bothwell,A.L.M., Paskind,M., Reth,M., Imanishi-Kari,T.,
            Rajewsky,K. and Baltimore,D.
  TITLE     Somatic variation of immunoglobulin light-chain genes: an
            experimental model for evolution by natural selection
  JOURNAL   Cell 24 (3), 625-637 (1981)
  MEDLINE   81196344
   PUBMED   6788374
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 164] from the original journal article.
            This sequence comes from Fig. 4.
FEATURES             Location/Qualifiers
     source          1..408
                     /organism="Balb/c sp."
                     /db_xref="taxon:10090"
     gene            1..408
                     /partial
                     /gene="IgM kappa chain variable region"
     CDS             1..408
                     /partial
                     /gene="IgM kappa chain variable region"
                     /note="hamster heart xenograft rejection associated; This
                     sequence comes from Fig. 4"
                     /codon_start=1
                     /product="IgM Kappa chain variable region"
                     /protein_id="AAB59891.1"
                     /db_xref="GI:1294410"
                     /translation="MEXXIVMSQAXXXXVXXGXXVXISCXASXSVSYMHWYQQKPGTSP
                     KRWIYLTSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFGSGTKL
                     EINRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT
                     DQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC"
BASE COUNT       89 a     85 c     88 g     76 t      1 others
ORIGIN

  Query Match             74.5%;  Score 295.2;  DB 10;  Length 408;
  Best Local Similarity   84.1%;  Pred. No. 1.1e-88;
  Matches  333;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy          1 ATGGATTCACAGGCCCAGGTTCTTATATTGCTCTGCTATGGGTATCTGGCACCTGTGGG 60
              |||.|| ||||| | |||| || ||  .  |||||||| ||||||.|||| ||||||||
Db          7 ATGGAATCACAGACACAGGTCCTCATGTCCCTGCTCTGGGTATCTGGTACCTGTGGC 66

Qy         61 GACATTGTGCTCACACAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 120
              ||||||.|| .||| ||| ||||    |.|| ||||      .|| |||| || ||||
Db         67 GACATTGTGATGACCCAGATCCCAGCTTCTGTGGCAGTAAGCCTAGGACAGAGGGCCACC 126

Qy        121 ATAAGCTGCAAAGCCAGCCAGAGTGTTGATTATGATGGTGATAGTTATATGAAC 175
              || |||||||| |||||||||||||  |  ||| |  || |  | ||||||||||
Db        127 ATGAGCTGCAAGTCCAGTCAGAGTGTTTTATACAGCTCCAACAATATAGAAC 181

Qy        176 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAAGTGCTGATTTACTGGGCATCCACTAGG 235
              |||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||||
Db        182 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAAGTGCTGATCTACTGGGCATCCACTAGG 241

Qy        236 GAATCCGGGGTCCCTGATCGCTTCATAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 295
              ||.|||| |||||||||||||||||  ||||||||||||||||||||||||||||| |||
Db        242 GAATCTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 301

Qy        296 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 355
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 361

Qy        356 CCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 396
              |||||||||||||||||||||||||||||||||||||||
Db        362 CCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 402


RESULT 14
MUSIGKV130
LOCUS       MUSIGKV130                339 bp    mRNA    linear   ROD 29-OCT-1994
DEFINITION  Mus musculus Ig rearranged kappa chain gene V19 J1 region.
ACCESSION   L16819
VERSION     L16819.1  GI:293622
KEYWORDS    V region; complementarity determining region; immunoglobulin light
            chain; kappa-immunoglobulin; processed gene.
SOURCE      Mus musculus (strain NZB/W F1) mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Lustgarten,D.L., Kavaler,J., Gerhard,W. and Scharff,M.D.
  TITLE     The response to a foreign antigen in the autoimmune NZB/W F1 murine
            strain
  JOURNAL   Unpublished (1993)
FEATURES             Location/Qualifiers
     source          1..339
                     /organism="Mus musculus"
                     /strain="NZB/W F1"
                     /db_xref="taxon:10090"
                     /cell_line="BW5 130"
                     /cell_type="hybridoma"
     gene            1..339
                     /gene="IgK V19"
     V_region        1..285
                     /gene="IgK-V19"
                     /standard_name="V19"
     misc_feature    70..102
                     /gene="IgK V19"
                     /standard_name="CDR1"
     misc_feature    148..168
                     /gene="IgK-V19"
                     /standard_name="CDR2"
     misc_feature    265..291
                     /gene="IgK V19"
                     /standard_name="CDR3"
     J_segment       286..324
                     /gene="IgK V19"
                     /standard_name="J1"
BASE COUNT       89 a     85 c     88 g     76 t      1 others
ORIGIN

  Query Match             74.5%;  Score 295;  DB 10;  Length 339;
  Best Local Similarity   92.3%;  Pred. No. 1.3e-88;
  Matches  310;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          61 GACATTGTGCTCACACAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 120
               |||||||| || |||||||||    |.|| ||||      .|| |||| || ||||
Db           1 GACATTGTGATGTCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACT 60

Qy         121 ATAAGCTGCAAAGCCAGTCAGAGTGTTGATTATGATGGTGATAGTTATATGAAC 175
               || |||||||| |||||||||||||  |  ||| |  || |  | ||||||||||
Db          61 ATGAGCTGCAAGTCCAGTCAGAGTGTTTTATACAGCTCCAACAATATAGAAC 115

Qy         176 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAAGTGCTGATTTACTGGGCATCCACTAGG 235
               |||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||||
Db         116 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAAGTGCTGATCTACTGGGCATCCACTAGG 175

Qy         236 GAATCCGGGGTCCCTGATCGCTTCATAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 295
               ||.|||| |||||||||||||||||  ||||||||||||||||||||||||||||| |||
Db         176 GAATCTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 235

Qy         296 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 355
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         236 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 295

Qy         356 CCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 396
               |||||||||||||||||||||||||||||||||||||||
Db         296 CCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 336
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RESULT 15
AF321954
LOCUS       AF321954                 336 bp    mRNA    linear   ROD 28-MAR-2002
DEFINITION  Mus musculus BW2 24-13 immunoglobulin light chain mRNA, partial
            cds.
ACCESSION   AF321954
VERSION     AF321954.1  GI:19697155
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 336)
  AUTHORS   Beger,E., Deocharan,B., Edelman,M., Erblich,B., Gu,Y. and
            Putterman,C.
  TITLE     A peptide DNA surrogate accelerates autoimmune manifestations and
            nephritis in lupus prone mice
  JOURNAL   J. Immunol. 168 (7), 3617-3626 (2002)
  MEDLINE   21964551
   PUBMED   11907127
REFERENCE   2  (bases 1 to 336)
  AUTHORS   Beger,E., Deocharan,B., Edelman,M. and Putterman,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2000) Division of Rheumatology, Albert Einstein
            College of Medicine, 1300 Morris Park Ave, Bronx, NY 10461, USA
FEATURES             Location/Qualifiers
     source          1..336
                     /organism="Mus musculus"
                     /strain="NZB x NZW F1"
                     /db_xref="taxon:10090"
                     /tissue_type="peptide-immunized"
     CDS             <1..>336
                     /codon_start=1
                     /product="BW2 24-13 immunoglobulin light chain"
                     /protein_id="AAL92950.1"
                     /db_xref="GI:19697156"
                     /translation="DIVMSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQ
                     KPGQSPELLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLYT
                     FGGGTKLEIK"
BASE COUNT      97 a     85 c     86 g     72 t
ORIGIN

  Query Match             74.8%;  Score 294.4;  DB 10;  Length 336;
  Best Local Similarity   92.9%;  Pred. No. 2e-88;
  Matches  312;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          61 GACATTGTGCTCACACAGTCTCCAGAATCTCTGGCTGTGTCTAAGGAGAAAGTCACT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GACATTGTGATGTCACAGTCTCATCATTCCTTGGCTGTGTCAGCAGGAGAAAGTTACT 60

Qy         121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ATGAGCTGCAAATCCAGTCAGAGTCTGTTATACAGTAGAAACCAAAGAAGAACTACTTGGCT 120

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAAGTGCTGATTTACTGGGCATCTACTAGG 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATCTT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATCTTATAATCTG 300
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Qy          61 GACATTGTGCTCACACAGTCTCCAGAATCTCTGGCTGTGTCTAAGGAGAAAGTCACT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GACATTGTGATGTCACAGTCTCATCATTCCTTGGCTGTGTCAGCAGGAGAAAGTTACT 60

Qy         121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ATGAGCTGCAAATCCAGTCAGAGTCTGTTATACAGTAGAAACCAAAGAAGAACTACTTGGCT 120

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAAGTGCTGATTTACTGGGCATCTACTAGG 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATCTT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATCTTATAATCTG 300
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Qy          61 GACATTGTGCTCACACAGTCTCCAGAATCTCTGGCTGTGTCTAAGGAGAAAGTCACT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GACATTGTGATGTCACAGTCTCATCATTCCTTGGCTGTGTCAGCAGGAGAAAGTTACT 60

Qy         121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ATGAGCTGCAAATCCAGTCAGAGTCTGTTATACAGTAGAAACCAAAGAAGAACTACTTGGCT 120

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAAGTGCTGATTTACTGGGCATCTACTAGG 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATCTT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATCTTATAATCTG 300
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Qy          61 GACATTGTGCTCACACAGTCTCCAGAATCTCTGGCTGTGTCTAAGGAGAAAGTCACT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GACATTGTGATGTCACAGTCTCATCATTCCTTGGCTGTGTCAGCAGGAGAAAGTTACT 60

Qy         121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ATGAGCTGCAAATCCAGTCAGAGTCTGTTATACAGTAGAAACCAAAGAAGAACTACTTGGCT 120

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAAGTGCTGATTTACTGGGCATCTACTAGG 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATCTT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATCTTATAATCTG 300
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Search completed: June 17, 2003, 19:19:14
Job time : 1346.22 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: June 17, 2003, 13:05:38 ; Search time 1617.93 Seconds
(without alignments)
6300.430 Million cell updates/sec

Title: US-09-249-011B-7
Perfect score: 396
Sequence: 1 atgaattcacaaaccaaqt.....gtaccaagctgaaaaaaaaaa 396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1e154866 seqs, 80927743476 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: qb_est1:*
10: qb_est2:*
11: qb_htc:*
12: qb_est3:*
13: qb_est4:*
14: qb_est5:*
15: em_esttim:*
16: em_estom:*
17: qb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	342.8	86.6	867	14	BQ930517	BQ930517 AGENCOURT
2	312	78.8	965	12	BP580837	BP580837 602995235
3	288.6	72.9	864	13	BI111610	BI111610 602895973
4	272.8	68.9	691	12	BF128999	BF128999 601811418
5	269.4	68.0	850	13	BG966217	BG966217 602840177
6	267	67.4	575	13	BI249452	BI249452 602995789
7	259.4	65.5	964	12	BG757628	BG757628 602727268
8	258.6	65.3	638	12	BG148633	BG148633 nu95b09.y
9	258.4	65.3	1199	14	BM804833	BM804833 AGENCOURT
10	256.8	64.8	700	14	BM788842	BM788842 K ES10061
11	256.6	64.8	798	12	BG426609	BG426609 602179775
12	256	64.6	641	10	AW405821	AW405821 UI-HF-BC0
13	255.2	64.4	984	14	BQ707260	BQ707260 AGENCOURT
14	253.4	64.0	643	10	AW590292	AW590292 CM2-S10108
15	251.8	63.6	904	14	BQ711273	BQ711273 AGENCOURT
16	251	63.4	886	12	BF674779	BF674779 602153783
17	244.2	62.9	633	12	BG542772	BG542772 602577734
18	247.6	62.5	508	10	AW406572	AW406572 HF-HF-BC0
19	247.6	62.5	819	12	BG686522	BG686522 602753471
20	247.6	62.5	842	12	BG757770	BG757770 602748882
21	247.6	62.5	887	12	BF663188	BF663188 602144432
22	247	62.4	473	14	BQ083970	BQ083970 K ES10147
23	247	62.4	492	14	BQ082708	BQ082708 K ES10144
24	247	62.4	625	13	BI824438	BI824438 603044716
25	247	62.4	849	14	BM769427	BM769427 K ES10052
26	247	62.4	876	12	BG397563	BG397563 602430662
27	245.6	62.0	921	12	BG569993	BG569993 602590249
28	245.4	62.0	527	14	BM821681	BM821681 K ES10090
29	245.4	62.0	710	12	BG537677	BG537677 602746021
30	244	61.6	384	13	AW515234	AW515234 ES10-0414
31	242.6	61.3	767	12	BG484518	BG484518 602605173
32	242.6	61.3	767	12	BG541967	BG541967 602594436
33	242.6	61.3	1057	12	BG539525	BG539525 602608152
34	242.4	61.2	769	12	BG534966	BG534966 602594155
35	242.2	61.2	761	12	BG538372	BG538372 602647975
36	241.4	61.0	925	12	BG298034	BG298034 602405954
37	241.2	60.9	698	13	BI760019	BI760019 603144177
38	240.6	60.8	573	12	BF128829	BF128829 601811615
39	240	60.6	745	12	BG484741	BG484741 602605627
40	239	60.4	495	11	BQ082810	BQ082810 K ES10144
41	239	60.4	661	11	BM831430	BM831430 K ES10053
42	239	60.4	665	11	BM768906	BM768906 K ES10051
43	235.8	59.5	541	12	BG547412	BG547412 602674783
44	234.4	59.2	869	12	BG429604	BG429604 602501285
45	234.2	59.1	559	12	BG548150	BG548150 602675691

ALIGNMENTS

RESULT 1
BQ930517
LOCUS BQ930517 867 bp mRNA linear EST 20-AUG-2002
DEFINITION AGENCOURT_8952297 NIH_3GAP_Sp24 Mus musculus cDNA clone IMAGE:6477099 5', mRNA sequence.
ACCESSION BQ930517
VERSION BQ930517.1 GI:22345548
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 867)
AUTHORS NIH MGC Project
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14018 row: i column: 04
High quality sequence stop: 710.
FEATURES Location/Qualifiers
source 1..867

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                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6477009"
                     /clone_lib="NCI_CGAP_Co21"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: colon; Vector: pCMV SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally.  Primer: oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT       227 a    239 c    207 g    191 t      3 others
ORIGIN

  Query Match             86.6%;  Score 342.8;  DB 14;  Length 867;
  Best Local Similarity   91.9%;  Pred. No. 1.7e-94;
  Matches  362;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          8 CGTATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGGGA 67
              ||:|||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGATCACAAGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGGGA 60

Qy         68 ATTGTGGATGTCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTAT 127
              |||||||||||||||||||  ||||||||||          ||||||| || |||||||
Db         61 CATTGTGATGTCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACTAT 120

Qy        128 TACTGCAAATCCAGTCAGATTCTGCTCAACAGTAGAACCCGAAGAACTACTTGGCTTG 187
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACTGCAAATCCAGTCAGATCTGCTCAACAGTAGAACCCGAAGAACTACTTGGCTTG 180

Qy        188 GTATCCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTATCCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGA 240

Qy        248 ATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC 307
              ||:||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        241 ATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC 300

Qy        308 AGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCAGCAATCTTATAATCCTTTA 367
              |||||| ||||||||||||||  ||||||||||||||||  |||||||||||||||| |
Db        301 AGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAAGCAATCTTATAATCCTCTG 360

Qy        368 TACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 403
              ||||||||  |||||| ||| ||||||||||
Db        361 TACTCGTTCGGCGGTGGGGACAAAGTTGGAAATAAAA 396


RESULT 2
BF580047
LOCUS       BF580047                 905 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602095425F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4209417 5',
            mRNA sequence.
ACCESSION   BF580047
VERSION     BF580047.1  GI:11653749
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 905)
  AUTHORS   NIH MGC http://mgc.nih.gov/
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM0275  row: I  column: 10
            High quality sequence stop: 757.

FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4209417"
                     /clone_lib="NCI_CGAP_Co24"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: colon; Vector: pCMV SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally.  Primer: oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT       248 a    236 c    217 g    204 t
ORIGIN

  Query Match             78.8%;  Score 312;  DB 12;  Length 905;
  Best Local Similarity   91.7%;  Pred. No. 5.3e-85;
  Matches  363;  Conservative    0;  Mismatches   30;  Indels    3;  Gaps    3;

Qy          1 ATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGG 60
              |||||||||||||||||||||||||||||||| |||||||||||||||||||  ||||||
Db          16 ATGGATTCACAGGCCCAGGTTCTTATA-TGCTGCTGCTATGGGTATCTGGCGCCTGTGGG 74

Qy         61 GACATTGTGGCTGACACAGTCTCCAGATTCCCTGGCTGTGAAGCTTAGGAGAGAGGGCCACT 120
              |||| |||| || ||||||||||  ||||||||||          ||||||| || ||||
Db         75 GACA-TGTGATGTCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACT 133

Qy        121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAGAACTACTTGGCTT 180
              || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 ATGAACTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAGAACTACTTGGCTT 193

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGG 240
              |||||||||||||||||  |||| ||||||||||||||||||||||||||||||||||||
Db        194 TGGTACCAGCAGAAACCA-GGGAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGG 252

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCA 300
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        253 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCA 312

Qy        301 TCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCAGCAATCTTATAATCCTTT 360
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 TCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAAGCAATCTTATAATCCTCT 372

Qy        361 TACACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 396
              |||||||||  |||||| ||| ||||||||||
Db        373 TACTCGTTCGGCGGTGGGGACAAAGTTGGAAATAAAA 410


RESULT 3
BI111610
LOCUS       BI111610                 864 bp    mRNA    linear   EST 26-JUN-2001
DEFINITION  602895974F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5025715 5',
            mRNA sequence.
ACCESSION   BI111610
VERSION     BI111610.1  GI:14502551
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 864)
  AUTHORS   NIH MGC http://mgc.nih.gov/
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Bentzinhansen Ph.D., Robin Humphreys
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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            Plate: LLAM1107  row: b  column: 20
            High quality sequence stop: 644.
FEATURES             Location/Qualifiers
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                     /db_xref "taxon:10090"
                     /clone "IMAGE:5025715"
                     /clone_lib "NCI_CGAP_Mam5"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage "7 months"
                     /lab_host "DH10B"
                     /note "organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Robin Humphreys,
                     NIH"
BASE COUNT     [illegible] a    233 c    156 g    205 t
ORIGIN

  Query Match             72.9%;  Score 288.6;  DB 13;  Length 864;
  Best Local Similarity   84.5%;  Pred. No. 8.2e-78;
  Matches  337;  Conservative    0;  Mismatches   59;  Indels    3;  Gaps    1;

Qy          1 [illegible] 60
Db          2 ATGGATTCACAGGCCCAGGTTCTTATGTTACTGCTGCTATGGGTTTCTGGTACCTGTGGG 61

Qy         61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACT 120
Db         62 GACATTGTAATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGATTACT 121

Qy        121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACACTAGAACCCGAGAGAACTACTTGGCT 180
Db        122 ATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTACCAATCAAAAGAACTACTTGGCC 181

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
Db        182 TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCATCCACTCGG 241

Qy        241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
Db        242 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 301

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCAATCTTATA   AT 357
Db        302 ATCAGTAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAACTAT 361

Qy        358 CTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
Db        362 [illegible]GGACTTTCGGTGGAGGTACCAAGCTGGAAATCAAA 400


RESULT 4
BF128999
LOCUS       BF128999                 691 bp    mRNA    linear   EST 24-OCT-2000
DEFINITION  601811818F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054205 5',
            mRNA sequence.
ACCESSION   BF128999
VERSION     BF128999.1  GI:10968039
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 691)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Lina Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM804  row: c  column: 06
            High quality sequence stop: 682.
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                     /db_xref "taxon:9606"
                     /clone "IMAGE:4054205"
                     /clone_lib "NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host "DH10B (phage-resistant)"
                     /note "organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected 500bp
                     for average insert size 1.8kb. Library constructed by Lina
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT     160 a    175 c    178 g    176 t      2 others
ORIGIN

  Query Match             68.9%;  Score 272.8;  DB 12;  Length 691;
  Best Local Similarity   80.6%;  Pred. No. 5.5e-73;
  Matches  319;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy          1 ATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGTACCTGTGGG 60
Db        170 ATGGTGTTGCAGACCCAGGTCTTCATTTCTCTGTTGCTCTGGATCTCTGGTGCCTACGGG 229

Qy         61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACT 120
Db        230 [illegible] 289

Qy        121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACACTAGAACCCGAGAGAACTACTTGGCT 180
Db        290 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 349

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
Db        350 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 409

Qy        241 [illegible] 300
Db        410 [illegible] 469

Qy        301 [illegible] 360
Db        470 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 529

Qy        361 [illegible]GGACCAAGGTGGAAATAAAA 396
Db        530 [illegible]CAAGCTGGAAATCAAA 565


RESULT 5
BG966217
LOCUS       BG966217                 850 bp    mRNA    linear   EST 11-JUN-2001
DEFINITION  [illegible] NCI_CGAP_Lu24 Mus musculus cDNA clone IMAGE:4508819 5',
            mRNA sequence.
ACCESSION   BG966217
VERSION     BG966217.1  GI:14353854
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 850)
```

```
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10991 row: j column: 20
            High quality sequence stop: 806.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4984013"
                     /sex="female"
                     /lab_host="DH10B (ElectroMax DH10B cells)"
                     /note="Organ: mammary gland; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size: 1.6 Kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP library."
BASE COUNT       222 a    222 c    192 g    214 t
ORIGIN

  Query Match             68.0%;  Score 269.4;  DB 14;  Length 850;
  Best Local Similarity   81.5%;  Pred. No. 6.6e-72;
  Matches  825;  Conservative    0;  Mismatches   21;  Indels    3;  Gaps    1;

Qy          1 ATGGATCCACAGGCCCAGGTTCTTATATTGGTGCTGCTATGGGTATCTGCTACCTGTGGG 60
              |||||||||||||||||||||||||| || ||||||||||||||||||| |||||||||
Db          9 ATGGATCCACAGGCCCAGGTTCTTATGTTACTGCTGCTATGGGTATCTGCTACCTGTGGG 68

Qy         61 GACATTGTGTCTGACTACTATCCTTCATTCTTTAAGTCTACCATCTCTGGAAGGCTGATT 120
              |||||| || || ||||||||||  ||||| |||||     | |||| |     |||
Db         69 GACATTGTGATGTCTCAGTCTCCACTCTCCCTGCCTGTCTCTCTTGGAGATCAAGCCTCT 128

Qy        121 ATCAGCTGCAGAGATCAGAGCCTTGTACACAGTAATGGAAACACCTACTTGAAT 180
              |||||||| |||||||| || || | | | | | | | | | | | | | | |||||||
Db        129 ATCAGATCTAGAGTCTACTTCTGAAGTTTTCTATCTTTCTGAATCAAAAGACTCTACTTGGCT 188

Qy        181 TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              ||| | |||||||||||||| || ||||||||||||||| |||||||| |||| ||||
Db        189 TGGTATCAGAAACCAGGACAGCCTCCTAAAGTTGTTATTTACTGGGCTTCTACTAGG 247

Qy        241 GAATCCGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
              |||||||| |||||||||| ||||   ||||||||||||||||||||||||||||||||
Db        248 GAATCTGGAGTCCCTGATCACTTCTCAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 307

Qy        301 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 360
              |||||||| |||||||||| |||| ||||||||||||||||||||||||||||||||||
Db        308 ATCAGCAGTCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 367

Qy        361 CCTTTCACGTTCGGCACAGGGACCAAGCTGGAAATAAAA 398
              |    |||||||||    |||||||| ||| | | |
Db        368 CCTCTCTTTGGTGCTGGGACCAAACTGGAGCTGAAA 405


RESULT 6
BG176452
LOCUS       BG176452                 525 bp    mRNA    linear   EST 17-OCT-2001
DEFINITION  602065760F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5151287 5',
            mRNA sequence.
ACCESSION   BG176452
VERSION     BG176452.1  GI:14776845
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11874 row: b column: 24
            High quality sequence stop: 525.
FEATURES             Location/Qualifiers
     source          1..525
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5151287"
                     /clone_lib="NCI_CGAP_Mam5"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="7 months"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Robin Humphreys,
                     NIH"
BASE COUNT       149 a    137 c    139 g    150 t
ORIGIN

  Query Match             67.4%;  Score 267;  DB 13;  Length 525;
  Best Local Similarity   82.7%;  Pred. No. 3.1e-71;
  Matches  330;  Conservative    0;  Mismatches   65;  Indels    4;  Gaps    2;

Qy          1 ATGGATCCACAGGCCCAGGTTCTTATGTTACTGCTGCTATGGGTATCTGCTACCTGTGGG 60
              |||||||||||||||||||||||||| || ||||||||||||||||||| |||||||||
Db          9 ATGGATCCACAGGCCCAGGTTCTTATGTTACTGCTGCTATGGGTATCTGCTACCTGTGGG 68

Qy         61 GACATTGTGTCTGACTACTATCCTTCATTCTTTAAGTCTACCATCTCTGGAAGGCTGATT 120
              |||||| || || ||||||||||  ||||| |||||     | |||| |     |||
Db         69 GACATTGTGATGTCTCAGTCTCCACTCTCCCTGCCTGTCTCTCTTGGAGATCAAGCCTCT 128

Qy        121 ATCAGCTGCAGAGATCAGAGCCTTGTACACAGTAATGGAAACACCTACTTGAAT 180
              |||||||| |||||||| || || | | | | | | | | | | | | | | |||||||
Db        129 ATCAGATCTAGAGTCTACTTCTGAAGTTTTCTATCTTTCTGAATCAAAAGACTCTACTTGGCT 188

Qy        181 TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              ||| | |||||||||||||| || ||||||||||||||| |||||||| |||| ||||
Db        189 TGGTATCAGAAACCAGGACAGCCTCCTAAAGTTGTTATTTACTGGGCTTCTACTAGG 247

Qy        241 GAATCCGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
              |||||||| |||||||||| ||||   ||||||||||||||||||||||||||||||||
Db        248 GAATCTGGAGTCCCTGATCACTTCTCAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 307

Qy        301 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 360
              |||||||| |||||||||| |||| ||||||||||||||||||||||||||||||||||
Db        308 ATCAGCAGTCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 367

Qy        361 CCTTTCACGTTCGGCACAGGGACCAAGCTGGAAATAAAA 398
              |    |||||||||    |||||||| ||| | | |
Db        368 CCTCTCTTTGGTGCTGGGACCAAACTGGAGCTGAAA 405


RESULT 7
BG757678
LOCUS       BG757678                 964 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602711206F1 NIH MGC_48 Homo sapiens cDNA clone IMAGE:4851521 5',
            mRNA sequence.
ACCESSION   BG757678
```

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VERSION     [illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 964)
  AUTHORS   NIH MGC Project [illegible]
  TITLE     National Institutes of Health: Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Rong/Rubin Laboratory
            cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: [illegible]
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: HuMI994  row: N  column: 18
            High quality sequence stop: 784.
FEATURES             Location/Qualifiers
     source          1..964
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4851621"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B cells from tonsils (cell line)"
                     /lab_host="DH10B (phage resistant)"
                     /note="Trans. Germinal B cells; Vector: pT7T3D-Pac
                     (Pharmacia) with a modified poly linker; Site_1: Not I;
                     Site_2: Eco RI; cDNA made by oligo-dT primer;
                     Directionally cloned into Eco RI/Xho I sites using the
                     following 5' adaptor: GGCACGAG(G). Size selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Rong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      236 a    280 c    238 g    210 t
ORIGIN

  Query Match           65.5%;  Score 259.4;  DB 12;  Length 964;
  Best Local Similarity   80.1%;  Pred. No. 8.3e-60;
  Matches  518;  Conservative    0;  Mismatches   76;  Indels    3;  Gaps    1;

Qy          3 GGATTCACAGGCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGGGGA 62
              || | ||| ||||||  | || | ||| |||| || | ||||  ||| ||||
Db          1 GGTGTTGCAGACCCAGGTCTTCATTTCTCCTTGCTCTGGATCCTCTGGTGGCTACGGGGA 60

Qy         63 CATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACTAT 122
              || ||| |||| |||||||||||| ||||||||||||    | || ||||||||||| ||
Db         61 CATCCTCATCAA CAGT CTCAGA CCTCCTCTCT GTG  AGCTCTGGAGCAGACTACTT 120

Qy        123 TACACTGCAAATCCAGTCAGAGTCTGCTCAACAATAGAAACCCGGAGAAACTACTTGGCTG 182
              | ||||| |||| |||||| |  | |||    ||  |  |||||||| ||||
Db        121 CAACTGCAAGTCCAGCCAGAGTCTCATCAACAGTAAAAACAAGAACTACTTAGCTTG 180

Qy        183 GTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGA 242
              | |||||||||||||| |||||||||| |||| || ||||||||| ||  ||||
Db        181 GTACTACAGAAACCAGGAGAGCCTCCTAAGCTGCTTATCTACTTTGCATCTACCGGGA 240

Qy        243 ATCCGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC 302
              || ||||||||||| || |||||||||| || |||||||||||||||||||||||||||||
Db        241 ATCCTGAGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATC 300

Qy        303 CAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAATCTTA---TAATCT 359
              ||||| |||||||||||| |||||||||||||||||||  |||| |||   || ||
Db        301 CAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCT 360

Qy        360 TTACACGTTCGGGGACAGGGGACCAAGCTGGAAATAAAA 396
              | ||||||| || |||||||||||||||| |||
Db        361 AAACACTTTCGGCCAAGGGACCAAGTTGGAAATCAAA 397

RESULT 8
BG148033
LOCUS       BG148033                 [illegible] bp    mRNA    linear   EST 01-FEB-2002
DEFINITION  [illegible] Soares_mouse_NMGb_bcell Mus musculus cDNA clone
            IMAGE:[illegible] similar to SW:KV1C_HUMAN P01614 IG KAPPA CHAIN
            V-IV REGION REI PRECURSOR, mRNA sequence.
ACCESSION   BG148033
VERSION     BG148033.1  GI:12652055
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   NCI-CGAP Project [illegible]
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGC:[illegible]
            Seq primer: 40KP from Gibco.
FEATURES             Location/Qualifiers
     source          1..300
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="Soares_mouse_NMGb_bcell"
                     /lab_host="DH10B (phage resistant)"
                     /note="Trans. Germinal B cells; Vector: pT7T3D-Pac
                     (Pharmacia) with a modified poly linker; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'
                     TGTTACGCAATCGAAGTGGGAGCGGCGCTGGTTTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized; constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT       85 a     72 c     79 g     64 t
ORIGIN

  Query Match           65.3%;  Score 258.4;  DB 12;  Length 300;
  Best Local Similarity   94.9%;  Pred. No. 9.2e-69;
  Matches  278;  Conservative    0;  Mismatches   14;  Indels    1;  Gaps    1;

Qy        105 AGGACAGACAGCAGCTACTATTACCTGCAAACTCAGTCTCAGACTCTGCCTCCACTGAC 164
              ||||||| || |||||| ||||||||||||.|||||||||||||||||||||||||||||
Db          1 ATGAGATGGTGCCTGCTCAGTTTCTTGGTCTTGTGGATCAAAGGTGAAAATGTGCTGACC 60

Qy        165 AGTGATAACTATGGCCTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTAC 224
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAGGAAACTATGTTCCTTGGTACCAGCAGAAGCCAGGACAGCCTCCTAAACTGCTGATCTAC 120

Qy        225 TGGGCATCCACTAGGGAATCCGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAG 284
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGGCATCCACTAGGGAATCCGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAG 180

Qy        285 ATTTCACTCTCACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAA 344
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATTTCACTCTCACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCAGCAA 240

Qy        345 TCTTATAATCTTTACACGTTCGGGGACAGGGGACCAAGCTGGAAATAAAA 396
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTTATAATCTTTACACGTTCGGAGCAGGGACCAAGCTGGAAATAAAA 292

RESULT 9
BM804933
LOCUS       BM804933                 1189 bp    mRNA    linear   EST 05-MAR-2002
```

```
DEFINITION  A BAC clone CTD-2327C7 NIH MGC 125 Homo sapiens cDNA clone IMAGE:5727543
            5', mRNA sequence.
ACCESSION   BM983843
VERSION     BM983843.1  GI:19121056
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1189)
  AUTHORS   NIH MGC http://mgc.nih.gov
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IMAM12716  row: j  column: 08
            High quality sequence stop: 465.
FEATURES             Location/Qualifiers
     source          1..1189
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5727543"
                     /clone_lib="NIH MGC 125"
                     /lab_host="DH10B"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.3 Kb, insert size range 1.5-5 Kb. Library is
                     normalized and enriched for full length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 836."
BASE COUNT      211 a    432 c    220 g    327 t
ORIGIN

  Query Match             65.8%;  Score 256.4;  DB 14;  Length 1189;
  Best Local Similarity   78.0%;  Pred. No. 1.8e-68;
  Matches  311;  Conservative    0;  Mismatches   89;  Indels    0;  Gaps    0;

Qy          1 ATGGGATCTAATCCTCAATTTGAATCTATGACTAAGTGTATAATGGACAATGAAGCTCCT 60
              ||||| |  || |||||||  ||| | |||  ||| | ||||  |||  |||  ||| |||
Db          1 ATGGGGCTCAGACCCAGGCTTCATTCTCTGTTGCCCTTGGATCTCTGGTGCCTATGGG 60

Qy         61 GACATTCATGTACAACAGTCTCAGATTCCTCCTCTAAGCTTACTAGAGAGGGCCACT 120
              |||||  |||  |||| ||||||||||| ||||||||||      | ||  ||||||||||
Db         61 GACATCCTGATCAACAGTCTCCAGACTCCCTGCTGCCCTGCCCAGAGGGCCACC 120

Qy        121 ATTAGCTTCAAAGTCAGTGCAGCTGCTAAAGCAAAGAAGCCAGCAGAAGCAGCACTGGCT 180
              ||| | |||||| |||||  || ||||     | | |  |||| | ||| |||
Db        121 ATCAACTTCAAGGTCAGCGCAGCTGCCAAGGCAAAGAAGCCAGCAGAAGCAGCACTGGCC 180

Qy        181 TGGTACAGCAAGACCTCCGAGGGCATGACCTCCGACCAGGTGGACAGCGACACCACAGCC 240
              |||||||||||  |||||||| ||||||||||| ||||| || ||||||||||| ||  ||
Db        181 TGGTACGCCAAGATCCAGCAGGCCCAGCTCGCCGGCAAGGCCACCGCCGAGATCGACAAG 240

Qy        241 GAATCCTCCGGCGACCTCATCAAGGAGCAGATCCTCGGCGCCAAGCCCGCCGAGATCGCC 300
              |||||  ||||||||||| || |||||||||| || |||| |||||||||||||||||
Db        241 GAAGCCTCCGGCGACCTCGCCAAGCAGATCCTCGGCGCCAAGCCCGCCGAGATCGCC 300

Qy        301 ATCGCCAGCCTCGCCAAGCTCGCCGCCCTCATCGTCGCCGGCAAGCTCATCAAGTCCTTC 360
              ||| ||| ||||||||||||| ||||  |||||||||||  |||| || | |  |  !
Db        301 ATCGCCGCCCTCGCCAAGGCCGGCGCCCTCGTCGCCGGCGAGCTCGTCAAGTCCTTC 360

Qy        361 TACAGCTTCTCGTACGAGGACCAGCTCGCCAACCTCATCAAG 396
                 ||  ||||  ||||||||||||||  || |||
Db        361 GACATCTTCGGCGGCGACGGCAAGGTCGGCATCAAG 396


RESULT 10
BM783842
LOCUS       BM783842                 700 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  K EST39961864 SI7N258215 Homo sapiens cDNA clone SI7N258215 2-C07
            5', mRNA sequence.
ACCESSION   BM783842
VERSION     BM783842.1  GI:19142074
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Choi,M.Y., Kim,M.K.,
            Oh,K.J., Cheong,J.E., Sohn,B.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: 082 42 860 4470
            Fax: 082 42 860 4409
            Email: yonsunq@mail.kribb.re.kr
            Plate: 2  row: C  column: 07
            High quality sequence stop: 700.
FEATURES             Location/Qualifiers
     source          1..700
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="SI7N258215-2-C07"
                     /clone_lib="SI7N258215"
                     /sex="M"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach, Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tobacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT selected mRNA by
                     priming with dT-tailed vector. The dT tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT      177 a    196 c    178 g    149 t
ORIGIN

  Query Match             64.8%;  Score 256.8;  DB 14;  Length 700;
  Best Local Similarity   78.0%;  Pred. No. 4.2e-68;
  Matches  306;  Conservative    0;  Mismatches   87;  Indels    0;  Gaps    0;

Qy          1 ATGGGATCTAATCCTCAATTTGAATCTATGACTAAGTGTATAATGGACAATGAAGCTCCT 60
              ||| |  ||| |||||||  | || |  ||| |||| ||| | | |  | |||  |||
Db          1 ATGAGGCTTCAGAGCCAGGCTTCATTCTCTGTTGCCCTTGGATCTCTGGTGCCTATGGG 60

Qy         61 GACATTCATGTACAACAGTCTCAGATTCCTCCTCTAAGCTTACTAGAGAGGGCCACT 120
              |||| ||| |||| ||||||||||| ||||||||||      | ||  ||||||||||
Db         61 GACATCCTGATCAACAGTCTCCAGACTCCCTGCTGCCCTGCCCAGAGGGCCACC 120

Qy        121 ATTAGCTTCAAAGTCAGTGCAGCTGCTAAAGCAAAGAAGCCAGCAGAAGCAGCACTGGCT 180
              ||| | |||||| |||||  || ||||     | | |  |||| | ||| |||
Db        121 ATCAACTTCAAGGTCAGCGCAGCTGCCAAGGCAAAGAAGCCAGCAGAAGCAGCACTGGCC 180

Qy        181 TGGTACAGCAAGACCTCCGAGGGCATGACCTCCGACCAGGTGGACAGCGACACCACAGCC 240
              |||||||||||  |||||||| ||||||||||| ||||| || ||||||||||| ||  ||
Db        181 TGGTACGCCAAGATCCAGCAGGCCCAGCTCGCCGGCAAGGCCACCGCCGAGATCGACAAG 240

Qy        241 GAATCCTCCGGCGACCTCATCAAGGAGCAGATCCTCGGCGCCAAGCCCGCCGAGATCGCC 300
              |||||  ||||||||||| || |||||||||| || |||| |||||||||||||||||
Db        241 GAAGCCTCCGGCGACCTCGCCAAGCAGATCCTCGGCGCCAAGCCCGCCGAGATCGCC 300

Qy        301 ATCGCCAGCCTCGCCAAGCTCGCCGCCCTCATCGTCGCCGGCAAGCTCATCAAGTCCTTC 360
              ||| ||| ||||||||||||| ||||  |||||||||||  |||| || | |  |  !
Db        301 ATCGCCGCCCTCGCCAAGGCCGGCGCCCTCGTCGCCGGCGAGCTCGTCAAGTCCTTC 360

Qy        361 TACAGCTTCTCGTACGAGGACCAGCTCGCCAACCTCATCAAG 396
                 ||  ||||  ||||||||||||||  || |||
Db        361 GACATCTTCGGCGGCGACGGCAAGGTCGGCATCAAG 396
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Qy          181 GGGIAGCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTATGGGCATGCCACTAGG 240
                ||||| ||||| |||| |||||||||| ||||| || ||| |||||| || ||
Db          211 GGGTAGCAGCAAAAACCAGGACAGCCTCCTAAACTGCTCATTACTGGCATCTATGCCGGC 270

Qy          241 GAATCTGGGGTCCCTGATCGCATTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
                |||||||||| |||||||||| || |||||||||| |||||||||| |||||||||| |||
Db          271 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGCTCTGGGACAGATTTCACTCTCACC 330

Qy          301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCAGCAATCTTATAATCTT 360
                |||||||| |||||||||||||| |||||||||||||||| ||| | |||| | |
Db          331 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 390

Qy          361 TACACGTTCGGCCAAGGGACCAAGGTGGAAATAAAA 396
                ||| |||| || |||| |||| |||| || |||
Db          391 CCCACTTTCGGCCAAGGGACCAAGCTGGAGATCAAA 426


RESULT 11
BG126836
LOCUS       BG126836                  756 bp    mRNA    linear   EST 14-MAY-2001
DEFINITION  yo42g07.r1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4606658 5',
            mRNA sequence.
ACCESSION   BG126836
VERSION     BG126836.1  GI:13432542
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 798)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: HCMI45  row: a  column: 08
            High quality sequence stop: 542.
FEATURES             Location/Qualifiers
     source          1..798
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4606658"
                     /clone_lib="NIH_MGC_75"
                     /tissue_type="kidney"
                     /lab_host="DH10B (11 phage resistant)"
                     /note="Organ: kidney; Vector: pBNK 11B (Clontech); Site 1:
                     SfiI (uncharacterized); Site 2: SfiI (uncharacterized); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-ACGGCCATIATGGGC-3' and 3' adaptor sequence:
                     5'-ATICIAGAGGCCGAGGCGGCCGACATG-dT(30)BN 3' (where B = A,
                     C, or G and N = A, C, G, or I).  Average insert size 1.65
                     kb (range 0.5-4.0 kb).  15/25 clones  picked  insert,
                     by PCR. This library was enriched for full length clones
                     and was constructed by Clontech Laboratories (Palo Alto,
                     CA). Note: this is a NIH MGC Library."
BASE COUNT      154 a    214 c    212 g    181 t
ORIGIN

  Query Match             64.8%;  Score 256.6;  DB 12;  Length 798;
  Best Local Similarity   79.4%;  Pred. No. 5.6e-68;
  Matches  311;  Conservative    0;  Mismatches   79;  Indels    3;  Gaps    1;

Qy            1 AIGGAIICACAGGCCAGCIICIIAIAIIGCIGCIGCIAIGGGIAICIGGCACCIGIGGG 60
                ||  || ||| |||||  | ||| |  ||| ||| || | |||| |||  |||
Db          561 ATCTGTCGCAGACCCAGCTCTTATTCCTGTTGCTGATCCTGTTGCCTATCGGG 616

Qy           61 GACAIIGIGCICACACAGICICCAGAIICCIGGCIGIAAGCIIAGCAGACAGGGCCACII 120
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```
                ||||| ||| |||| |||||||||| ||||||||||     | || ||||||||||
Db           91 GACAGCGTCATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 150

Qy          121 AIIAACIGCAAAAGCAGCCAGAGIGIIIIAIAGCICCAACAATAAGAACIACIIAGCII 180
                || | ||||| |||| |||||| | |  ||| |  | |  |||||||||| | |
Db          151 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 210

Qy          181 TGGIACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTATTGGGCATCCACTAGG 240
                |||||||||| |||||||| |||||||||||||||| || | ||||||||| ||  ||
Db          211 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAACTGCTCTATTTCCTGGGCATCTACCGGG 270

Qy          241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
                ||||| |||||||||| || |||||||||| || |||||||||| |||||||||| |||
Db          271 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGCTCTGGGACAGATTTCACTCTCACC 330

Qy          301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCAGCAATCTTATA   AT 357
                |||||||||||||||||||| |||||||||||||||| ||||  |||| |   |
Db          331 ATCAGCAGTCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 390

Qy          358 TTACACGTTCGGCCAAGGGACCAAGGTGGAAATAAAA 396
                || |||| || |||| |||| |||| || |||
Db          391 CCCACTTTCGGCCAAGGGACCAAGCTGGAGATCAAA 429


RESULT 12
AW405821
LOCUS       AW405821                  641 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  OI HF B16-abp h 07 9 01.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3057636 5', mRNA sequence.
ACCESSION   AW405821
VERSION     AW405821.1  GI:6924878
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 641)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Rec'd 81 site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares lab
            cDNA Library Arrayed by: M.B. Soares lab
            DNA Sequencing by: M.B. Soares lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov/image.html
            Sequencer: M13 forward.
FEATURES             Location/Qualifiers
     source          1..641
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3057636"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGCH5"
                     /lab_host="DH10B (111)"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      159 a    128 c    195 g    141 t
ORIGIN

  Query Match             64.8%;  Score 256.6;  DB 12;  Length 641;
  Best Local Similarity   81.0%;  Pred. No. 7.9e-68;
  Matches  311;  Conservative    0;  Mismatches   73;  Indels    3;  Gaps    1;
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RESULT 13
Bg*****
LOCUS Bg****** 984 bp mRNA linear EST 26-JUL-2002
DEFINITION AGENCOURT 8435459 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277745 5', mRNA sequence.
ACCESSION Bg******
VERSION Bg******.1 GI:12846159
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 984)
AUTHORS NIH MGC http://www.ncbi.nlm.nih.gov
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Invitrogen Laboratory
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Primer: Lic*M.494 row: j column: 18
High quality sequence stop: 729.

FEATURES Location/Qualifiers
source 1..984
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6277745"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo dT primer, directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGAATTCGAG(G). Library constructed by Kind Nong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC library."

BASE COUNT 242 a 229 c 242 g 271 t 5 others
ORIGIN

Query Match 64.4%; Score 255.2; DB 14; Length 984;
Best Local Similarity 77.8%; Pred. No. 1.6e-67;
Matches 308; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 1 ATGGATTTATCAGGCCAGATTTTTATATTCTGCTGCTATGGGTATTTGGCAGCTGTGGG 60
Db 21 ATGGTGTTGCAGACCCAGGTCTTCATTTCTCTGTTGCTCTGGATCTCTGGTGCTACGGG 80

Qy 61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACT 120
Db 81 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTAGGCGAGAGGGCCACC 140

Qy 121 ATTAACTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGACAAACTACTTAGCT 180
Db 141 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATTCATCTCCAATAATAAGAACTACTTAGCT 200

Qy 181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATTACTGGGCATCCTACTAGG 240
Db 201 TGGTACCAGCAGAAAGCAGGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCCGG 260

Qy 241 GAATCCGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
Db 261 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 320

Qy 301 ATCAGCAGTCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATCTTGCTACT 360
Db 321 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATCTTGCTACT 380

Qy 361 TACGGCCAGGGGACCAAGGTGGAAATAAAA 396
Db 381 TACGGCGGAGGGACCAAGGTGGAAATCAAA 416

RESULT 14
AW390292
LOCUS AW390292 643 bp mRNA linear EST 04-FEB-2000
DEFINITION CM2_SI0182_221099_023_104_SI0182 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW390292
VERSION AW390292.1 GI:6894951
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 643)
AUTHORS BCGP http://www.ludwig.org.br/ZORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo SP, Brazil
Tel: +55-11 2704922
Fax: +55-11 2787001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
http://www.ludwig.org.br/cgi-bin/db/dbbrowse?CM2_SI0182_221099_023_104&13_1999_10_22&14_1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 641.

FEATURES Location/Qualifiers
source 1..643
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="SI0182"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini library was made by cloning products derived from ZORESTES PCR (U.S. Letters Patent application

```
                   No. 196,716 Ludwig Institute for Cancer Research)
                   profiles into the pUC 18 vector. Reverse transcription of
                   tissue mRNA and cDNA amplification were performed under
                   low stringency conditions."
BASE COUNT      162 a    173 c    162 g    146 t
ORIGIN

  Query Match             64.0%;  Score 253.4;  DB 10;  Length 643;
  Best Local Similarity   78.9%;  Pred. No. 4.9e-67;
  Matches  315;  Conservative    0;  Mismatches   81;  Indels    3;  Gaps    1;

Qy          1 ATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGG 60
Db          9 ATGGTGTTGCAGACCCAGGTCTTCATTTCTCTGTTGCTCTGGATCTCTGGTGCCTACGGG 68

Qy         61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACT 120
Db         69 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 128

Qy        121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCGAGAGAACTACTTGGCT 180
Db        129 ATCAACTGCAAGTCCAGCCAGAGTATTTTATACAACTCCAAAAATAAGAACTACTTAGCT 188

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
Db        189 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCTTTTACTGGGCATCTACGCGG 248

Qy        241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
Db        249 AAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGCGACAGATTTCACTCTCACC 308

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAATCTTATA   AT 357
Db        309 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTTTAGTCAT 368

Qy        358 CTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
Db        369 CCTCAAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 407


RESULT 15
BQ711273
LOCUS       BQ711273                 904 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8354747 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278306
            5', mRNA sequence.
ACCESSION   BQ711273
VERSION     BQ711273.1  GI:21850172
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 904)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2466  row: b  column: 03
            High quality sequence stop: 579.
FEATURES             Location/Qualifiers
     source          1..904
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6278306"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH MGC Library."
BASE COUNT      208 a    264 c    219 g    212 t      1 others
ORIGIN

  Query Match             63.6%;  Score 251.8;  DB 14;  Length 904;
  Best Local Similarity   78.7%;  Pred. No. 1.8e-66;
  Matches  314;  Conservative    0;  Mismatches   82;  Indels    3;  Gaps    1;

Qy          1 ATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGG 60
Db          3 ATGGTGTTGCAGACCCAGGTCTTCATTTCTCTGTTGCTCTGGATCTCTGGTGCCTACGGG 62

Qy         61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACT 120
Db         63 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 122

Qy        121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCGAGAGAACTACTTGGCT 180
Db        123 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 182

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
Db        183 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 242

Qy        241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
Db        243 GAATCTGGGGTCCCTGACCGCTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 302

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAATCTTA   TAAT 357
Db        303 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTAGT 362

Qy        358 CTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
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Search completed: June 17, 2003, 19:59:20
Job time : 1022.93 secs
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GenCore version 5.1.6
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QM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 14:02:0 ; Search time 174.47 Seconds
(without alignments)
5619.472 Million cell updates/sec

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Perfect score: 440
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2867259 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 5734518

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	440	100.0	396	21	AAA59695	DNA encoding light
2	365.8	83.1	396	21	AAA59694	Nucleotide sequence
3	340	86.9	480	10	AAN01663	Light chain of mon
4	332	84.8	952	16	AAQ94036	MAb 55.1 light cha
5	301.4	76.1	439	18	AAI60729	cDNA encoding huma
6	301.4	76.1	439	18	AAI60733	cDNA encoding huma
7	298.2	75.3	399	15	AAQ66645	Sequence encoding
8	293.6	74.1	402	18	AAI14415	Xenograft antibody
9	288.6	72.9	399	17	AAQ74067	Monoclonal antibod
10	288.6	72.9	439	18	AAI60734	cDNA encoding wild
11	286.8	72.4	418	17	AAI34152	Monoclonal antibod
12	285.4	72.1	439	18	AAI72268	Chimeric MAb 1F 87
13	285.4	72.1	468	19	AAI72269	Mouse MAb 1F light
14	283.2	71.5	342	20	AAX34465	Mouse MAb 6A4 high
15	279.6	70.7	1443	15	AAQ62958	Glycophorin antibo
16	279	70.5	427	20	AAZ42779	Murine monoclonal
17	279	70.5	8068	20	AAZ42781	pKN100 E19 chimeri
18	278.8	70.4	746	21	AAZ28062	Human anti-glycoph
19	272.8	68.9	742	15	AAV36287	DNA coding Fv ESM wh
20	275.8	69.6	870	15	AAQ62956	Glycophorin antibo
21	275.2	69.5	660	14	AAQ54480	Sequence encoding
22	270.8	68.4	330	19	AAV28978	Anti-DNA II/IM (Hu
23	270.6	68.3	864	20	AAV72072	Fusion protein p37
24	270.6	68.3	2019	20	AAV72059	Plasmid pN34/5-cis
25	270.6	68.3	2025	20	AAV72064	Fusion protein pN6
26	267.2	67.5	336	20	AAX34588	Mouse MAb 6A4 muta
27	267.2	67.5	1701	13	AAQ59919	pMDR1000 insert.
28	267.2	67.5	1701	13	AAQ59920	Vector pMDR1000.
29	264.4	66.8	404	22	AAE81011	Anti-CA125 brinant
30	261.4	66.1	438	9	AAN80499	Encodes V region o
31	260.8	65.9	511	20	AAV86720	PCR clone AY241.
32	257.4	65.0	398	15	AAQ66669	pKEG 200 Ab light
33	257.4	65.0	756	13	AAQ63842	Encodes VKappa reg
34	256.2	64.7	423	20	AAX96625	Human monoclonal a
35	255	64.4	792	25	ABQ36219	Human ovarian anti
36	255	64.4	1033	23	AAS60145	Human cDNA clone H
37	253.6	64.0	468	21	AAQ98443	Human colon cancer
38	250.2	63.2	407	13	AAQ26047	Version of Lohai
39	248.6	62.8	402	16	AAT60780	E-selectin specifi
40	248.6	62.8	9069	20	AAZ42784	pKN100 human resha
41	248.2	62.7	444	13	AAQ30980	Insert pMDR1003.
42	247	62.4	5783	17	AAZ31121	Anti-IL-5 humanise
43	247	62.4	8783	19	AAV92694	Plasmid pCNIL5HZ167
44	244.4	61.7	744	21	AAA77243	M-CSF-R EV fragmen
45	244.4	61.7	774	24	AAS97144	P5-23 single chain

ALIGNMENTS

RESULT 1
AAA59695
ID AAA59695 standard; DNA; 396 BP.
XX
AC AAA59695;
XX
DT 11-NOV-2000 (first entry)
XX
DE DNA encoding light chain variable region of 5E1 antibody.
XX
KW EP1031619-B; 5E1; B7 molecule; B7; humanised immunoglobulin;
KW autoimmune disease; infectious disease; inflammatory disorder;
KW transplant; graft versus host disease; allergic reaction; asthma;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome; ss.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..396
FT /*tag = a
FT /product= "light chain variable region of 5E1 antibody"
FT /note= "no termination codon given"
FT sig_peptide 1..60
FT /*tag = b
FT mat_peptide 61..396
FT /*tag = c
XX

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PN   WO200047625-A2.
XX
PD   17-AUG-2000.
XX
PF   09-FEB-2000; 2000WO-US03303.
XX
PR   12-FEB-1999;   99US-0249011.
PR   24-JUN-1999;   99US-0336506.
XX
PA   (GEMY ) GENELABS INST INC.
XX
PI   Co MS;  Vasquez M;  Carreno B;  Celniker AC;  Collins M;  Goldman S;
PI   Gray GS;  Knight A;  O'Hara D;  Rup B;  Veldman GM;
XX
DR   WPI; 2000-524542/47.
DR   P-PSDB; AAB07964.
XX
PT   Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT   from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT   modulates immune responses and can therefore treat e.g. autoimmune
PT   diseases, infectious diseases
XX
PS   Example 1; Fig 1B; 162pp; English.
XX
CC   The present sequence encodes the light chain variable region of the
CC   murine antibody 4D1. The antibody has a binding specificity to B7
CC   molecules. The antibody is used to construct humanized immunoglobulins,
CC   which comprise an antigen binding region of non human origin and a
CC   portion of a human immunoglobulin. The humanized immunoglobulins are
CC   useful for treating autoimmune diseases, infectious diseases,
CC   inflammatory disorders, systemic lupus erythematosus, diabetes
CC   mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC   inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC   also useful for treating a transplant recipient or preventing transplant
CC   rejection in a transplant recipient, and treating proliferative disease
CC   (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC   thalassemia and aplastic anaemia), inborn errors of metabolism,
CC   congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ   Sequence 896 BP; 98 A; 97 C; 104 G; 97 T; 0 other;

  Query Match             91.1%;  Score 460.8;  DB 21;  Length 896;
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```
RESULT 2
AAA59693
ID   AAA59693 standard; DNA; 896 BP.
XX
AC   AAA59693;
XX
DT   14-NOV-2000  (first entry)
XX
DE   Nucleotide sequence of light chain variable region of 4D1 antibody.
XX
KW   Antibody 4D1; B7 molecule; B7; humanised immunoglobulin;
KW   autoimmune disease; infectious disease; inflammatory disorder;
KW   systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW   arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW   multiple sclerosis; transplant rejection; proliferative disease;
KW   leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW   aplastic anaemia; myeloid dysplasia syndrome; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..396
FT                   /*tag= a
FT                   /product= "light chain variable region of 4D1 antibody"
FT                   /note= "no termination codon given"
FT   sig_peptide     1..60
FT                   /*tag= b
FT   mat_peptide     61..396
FT                   /*tag= c
XX
PN   WO200047625-A2.
XX
PD   17-AUG-2000.
XX
PF   09-FEB-2000; 2000WO-US03303.
XX
PR   12-FEB-1999;   99US-0249011.
PR   24-JUN-1999;   99US-0336506.
XX
PA   (GEMY ) GENELABS INST INC.
XX
PI   Co MS;  Vasquez M;  Carreno B;  Celniker AC;  Collins M;  Goldman S;
PI   Gray GS;  Knight A;  O'Hara D;  Rup B;  Veldman GM;
XX
DR   WPI; 2000-524542/47.
DR   P-PSDB; AAB07964.
XX
PT   Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT   from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT   modulates immune responses and can therefore treat e.g. autoimmune
PT   diseases, infectious diseases
XX
PS   Example 1; Fig 1B; 162pp; English.
XX
CC   The present sequence encodes the light chain variable region of the
CC   murine antibody 4D1. The antibody has a binding specificity to B7
CC   molecules. The antibody is used to construct humanized immunoglobulins,
CC   which comprise an antigen binding region of non human origin and a
CC   portion of a human immunoglobulin. The humanized immunoglobulins are
CC   useful for treating autoimmune diseases, infectious diseases,
CC   inflammatory disorders, systemic lupus erythematosus, diabetes
CC   mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC   inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC   also useful for treating a transplant recipient or preventing transplant
CC   rejection in a transplant recipient, and treating proliferative disease
CC   (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC   thalassemia and aplastic anaemia), inborn errors of metabolism,
CC   congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ   Sequence 896 BP; 98 A; 97 C; 104 G; 97 T; 0 other;

  Query Match             91.1%;  Score 460.8;  DB 21;  Length 896;
```

Best local similarity: 94.4%; Prob. No. 1e-107;
Matches 471; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

RESULT 3
AAN91993
ID AAN91993 standard; DNA; 480 BP.
XX
AC AAN91993;
XX
DT 14-MAR-1990 (first entry)
XX
DE Light chain of monoclonal antibody 6A4.
XX
KW Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP I.
XX
FH Key Location/Qualifiers
FT CDS 37..480
FT /*tag= a
XX
PN EP338995-A.
XX
PD 25-OCT-1989.
XX
PF 12-APR-1989; 89EP-0106463.
XX
PR 19-APR-1988; 88DE-3813023.
XX
PA (BEHW) BEHRINGWERKE.
XX
PI Domdey H, Manuel M, von Specht BU;
XX
DR WPI; 1989-321861/45.
DR P-PSDB; AAP93078.
XX
PT Monoclonal antibody to Pseudomonas aeruginosa and DNA coding for
PT variable antibody regions.
XX
PS Claim 1; page 52; 72pp; German.
XX
CC The sequence has a variable and constant region. Monoclonal antibody 6A4
CC reacts with the OMP I protein of all 19 known serotypes of P.aeruginosa.
CC It is used for therapy and diagnosis of infection, and as a carrier for
CC drugs. The antibody is IgG2a subclass.
XX

SQ Sequence 480 BP; 115 A; 118 C; 135 G; 112 T; 0 other;

Query Match 85.0%; Score 846; DB 1; Length 480;
Best local similarity 91.2%; Prob. No. 7.1e-101;
Matches 461; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

RESULT 4
AAQ94036
ID AAQ94036 standard; cDNA; 952 BP.
XX
AC AAQ94036;
XX
DT 21-NOV-1995 (first entry)
XX
DE MAb 55.1 light chain cDNA.
XX
KW Antigen binding structure; complementarity determining region; CDR;
KW CA55.1; colorectal cancer; tumor associated antigen; hybridoma;
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 16..735
FT /*tag= a
FT sig_peptide 16..75
FT /*tag= b
FT mat_peptide 76..732
FT /*tag= c
XX
PN WO9515382-A.
XX
PD 08-JUN-1995.
XX
PF 29-NOV-1994; 94WO-GB02610.
XX
PR 03-DEC-1993; 93GB-0024451.
XX
PA (ZENE) ZENECA LTD.
XX
PI Blakey DC, Boyd C, Copley CG, Hall SM, Paterson DS;

```
RI   Rose MS;  Wright AI.
XX
RN   WPI; 1996-215229/29.
RP   P PSDB; AAW10544.
XX
PT   Antigen binding structures containing CDRs recognising the CA55.1
PT   antigen - produced by hybridomas and host cells, for use in the
PT   diagnosis and therapy of cancer
XX
PS   Disclosure; Fig.1b; 121pp; English.
XX
CC   MAb 55.1 (ECACC 96081901) recognises the colorectal tumor associated
CC   antigen CA55.1.  cDNAs for the heavy (AAQ94037) and light (AAQ94036)
CC   chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or
CC   V-gen humanized 55.1 constructs have been expressed in myeloma
CC   cells and E. coli.
XX
SQ   Sequence 952 BP; 215 A; 268 C; 215 G; 254 T; 0 other;

  Query Match             84.8%;  Score 342;  DB 1;  Length 952;
  Best Local Similarity   89.9%;  Pred. No. 3.6e-98;
  Matches  453;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTGCTATTTTAAAAGGTGTCCAGTGTGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTGCTATTTTAAAAGGTGTCCAGTGTGAG 60

Qy         61 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAGGTCCCTGAGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAGGTCCCTGAGACTC 120

Qy        121 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGGCAAGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGGCAAGCT 180

Qy        181 CCAGGGAAGGGCCTGGAGTGGGTCTCAGCTATTAGTTGGAATAGTGGTAGCATAGGCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGGGAAGGGCCTGGAGTGGGTCTCAGCTATTAGTTGGAATAGTGGTAGCATAGGCTAT 240

Qy        241 GCGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTAT 300

Qy        301 CTGCAAATGAACAGTCTGAGAGCTGAGGACACGGCCTTGTATTACTGTGCAAAAGATAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGCAAATGAACAGTCTGAGAGCTGAGGACACGGCCTTGTATTACTGTGCAAAAGATAAA 360

Qy        361 GGTATAGCAGCAGCTGGTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTATAGCAGCAGCTGGTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTC 420

Qy        421 AG 422
              ||
Db        421 AG 422


RESULT 2
AAI96720
ID   AAI96720 standard; cDNA; 439 BP.
XX
AC   AAI96720;
XX
DT   2-SEP-1997  (first entry)
XX
DE   cDNA encoding humanised murine anti E-selectin antibody CY1788V(1A).
XX
KW   Humanised; murine; mouse; E-selectin; antibody; light chain;
KW   variable region; detection; inhibition; mediation; cell adhesion;
KW   diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
KW   acute respiratory distress syndrome; stress cystic breast disease;
KW   cancer; treatment; splanchnic occlusion shock; psoriasis;
KW   complement; chimeric; ds.
XX
OS   Chimeric - Mus spp.
OS   Element - Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             16..426
FT                   /*tag= a
FT                   /note= "no stop codon given"
XX
PN   WO9640942-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US09204.
XX
PR   07-JUN-1995;   95US-0482112.
XX
PA   (CYTE ) CYTEL CORP.
XX
PI   Bendig MM;  Jones ST;  Perez C;  Saldanha JW;  Williams MA;
PI   Jones S;
XX
DR   WPI; 1997-077272/07.
DR   P-PSDB; AAW10544.
XX
PT   Humanised anti E-selectin antibody - useful for diagnosis and
PT   treatment of, e.g. inflammatory responses, septic shock, acute
PT   respiratory distress syndrome or cancer
XX
PS   Claim 29; Page 69; 89pp; English.
XX
CC   The present sequence encodes the humanised murine anti E-selectin
CC   antibody (Ab) light chain variable region, CY1788V(1A). The Ab can
CC   be used to detect E-selectin, or inhibit E-selectin mediated cell
CC   adhesion. It can also be used to diagnose, reduce or inhibit an
CC   inflammatory response, or the severity of pathologies, e.g. septic
CC   shock, acute respiratory distress syndrome, wound associated
CC   sepsis, stress cystic breast disease or cancer, or treat, e.g.
CC   splanchnic occlusion shock, or psoriasis. It can be administered to
CC   a human without inducing an immune response, in addition, the
CC   effector portion of the Ab can interact with various components of
CC   the human immune system, including complement.
XX
SQ   Sequence 439 BP; 106 A; 110 C; 117 G; 106 T; 0 other;

  Query Match             76.1%;  Score 301.4;  DB 1;  Length 439;
  Best Local Similarity   86.5%;  Pred. No. 2.8e-88;
  Matches  345;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    1;

Qy          1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTGCTATTTTAAAAGGTGTCCAGTGTGAG 60
              ||||| ||||||  |||||| || | |  |||||| | ||||||||||| ||||||||||
Db         28 ATGGAGTCAGTTCTGAGGTCCTGATGTCCTGTTGGTCTATATCTGGTATACTGTGTGGGG 87

Qy         61 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAGGTCCCTGAGACTC 120
              |||||||||| |||||||||||||||| ||||||||||     | || ||||||||| ||
Db         88 GAGGTGAAGCTGATGGAGTCTGGAGGTGGCCTGGTGCAGCCTGGGGGATCCCTGAAACTC 147

Qy        121 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGGCAAGCT 180
              || | |||||| ||||||||||||||| | ||||| ||| | | ||||||||||| |
Db        148 TCATGTGCAGCCTCTGGATTCATTTTTAGTAATGCTTGGATGAACTGGGTCCGCCAGGCT 207

Qy        181 CCAGGGAAGGGCCTGGAGTGGGTCTCAGCTATTAGTTGGAATAGTGGTAGCATAGGCTAT 240
              |||||||||||||||||||||||||||||||| || ||||||||||||||||||| |||
Db        208 CCAGGAAAGGGTCTAGAGTGGATTTCAGCTATTAGTTGGAATAGTGGTAGCATAGGCTAT 267

Qy        241 GCGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTAT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GCGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCCTGTAT 327

Qy        301 CTGCAAATGAACAGTCTGAGAGCTGAGGACACGGCCTTGTATTACTGTGCAAAAGATAAA 360
              |||||||||||||||||||||||||||||||||||||||||||||  || |||| ||||
Db        328 CTGCAGATGAACAGCCTGAAAGCTGAGGACACTGCCGTGTATTACTGTGCAAGACTAAA 387

Qy        361 GGTATAGCAGCAGCTGGTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 GGTCTCACAGTTGGGTCAAGGACCAAGGTGGACATAAAA 426
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RESULT 6
AAT[illegible]
ID   AAT[illegible] standard; cDNA; 439 BP.
XX
AC   AAT[illegible];
XX
DT   25-SEP-1997  (first entry)
XX
DE   cDNA encoding humanised murine anti E-selectin antibody CY1788V(LB).
XX
KW   Humanised; murine; mouse; E-selectin; antibody; light chain;
KW   variable region; detection; inhibition; mediation; cell adhesion;
KW   diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
KW   acute respiratory distress syndrome; gross cystic breast disease;
KW   cancer; treatment; splanchnic occlusion shock; psoriasis;
KW   complement; chimeric; ds.
XX
OS   Chimeric   Mus spp.
OS   Chimeric   Homo sapiens.
OS   Synthetic.
XX
FH   Key              Location/Qualifiers
FT   CDS              16..426
FT                    /*tag=  a
FT                    /note= "no stop codon given"
XX
PN   WO9640942-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;    96WO-US09204.
XX
PR   07-JUN-1995;    95US-0482112.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Bendig MM,  Jones ST,  Perez C,  Saldanha JW,  Williams MA;
PI   Jones S;
XX
DR   WPI; 1997-[illegible]/0?.
DR   P-PSDB; AAW[illegible].
XX
PT   Humanised anti E-selectin antibody - useful for diagnosis and
PT   treatment of, e.g. inflammatory responses, septic shock, acute
PT   respiratory distress syndrome or cancer
XX
PS   Claim 2?; Page 71; 89pp; English.
XX
CC   The present sequence encodes the humanised murine anti E-selectin
CC   antibody (Ab) light chain variable region, CY1788V(LB). The Ab can
CC   be used to detect E-selectin, or inhibit E-selectin mediated cell
CC   adhesion. It can also be used to diagnose, reduce or inhibit an
CC   inflammatory response, or the severity of pathologies, e.g. septic
CC   shock, acute respiratory distress syndrome, wound associated
CC   sepsis, gross cystic breast disease or cancer, or treat, e.g.
CC   splanchnic occlusion shock, or psoriasis. It can be administered to
CC   a human without inducing an immune response, in addition, the
CC   effector portion of the Ab can interact with various components of
CC   the human immune system, including complement.
XX
SQ   Sequence 439 BP; 106 A; 110 C; 118 G; 105 T; 0 other;

  Query Match             76.1%;  Score 301.4;  DB 18;  Length 439;
  Best Local Similarity   86.5%;  Pred. No. 2.8e-88;
  Matches  345;  Conservative    0;  Mismatches   51;  Indels    3;  Gaps    1;

Qy          1 [illegible] 60
Db         28 [illegible] 87

Qy         61 [illegible] 120
Db         88 GACATTGTGATGACACAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 147

Qy        121 [illegible] 180
Db        148 [illegible] 207

Qy        181 [illegible] 240
Db        208 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAGCTGTTGATCTACTGGGCATCCACTAGG 267

Qy        241 [illegible] 300
Db        268 [illegible] 327

Qy        301 [illegible] 357
Db        328 [illegible] 387

Qy        358 [illegible] 396
Db        388 [illegible] 426


RESULT 7
AAQ66845
ID   AAQ66845 standard; DNA; 399 BP.
XX
AC   AAQ66845;
XX
DT   31-DEC-1994  (first entry)
XX
DE   Sequence encoding the light chain variable region of the mouse NA-8
DE   antibody, including the signal sequence and mature chain.
XX
KW   Antibody NA-8; human CD18; complementarity determining region; CDR;
KW   ss.
XX
OS   Mus musculus.
XX
FH   Key              Location/Qualifiers
FT   CDS              1..399
FT                    /*tag=  a
XX
PN   WO9412214-A.
XX
PD   09-JUN-1994.
XX
PF   30-NOV-1993;    93WO-US11611.
XX
PR   01-DEC-1992;    92US-0983949.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Co MS,  Landolfi NF;
XX
DR   WPI; 1994-199973/24.
DR   P-PSDB; AAR59509.
XX
PT   New humanised antibodies specific for CD18 - derived from new
PT   murine antibody NA 8, prevent binding of neutrophils to
PT   endothelial cells, useful for treating inflammation
XX
PS   Disclosure; Fig 1A; 50pp; English.
XX
CC   The mouse antibody NA-8 binds to human CD18. cDNAs for the heavy
CC   chain and light chain variable domain genes of NA-8 were cloned
CC   using anchored PCR. The cDNA variable domain sequences and the
CC   deduced AA sequences are shown in AAQ66845/R59509 and AAQ66846/R59510.
XX
SQ   Sequence 399 BP; 102 A; 88 C; 100 G; 109 T; 0 other;

  Query Match             75.0%;  Score 298.2;  DB 15;  Length 399;
  Best Local Similarity   86.0%;  Pred. No. 3e-87;
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  Matches  414;  Conservative    0;  Mismatches   54;  Indels    3;  Gaps    1;

Qy          1 ATGGAGACCACAGTCAGGCTCCTAGTATTTCTTCTGCTACTGTGGTTAATGGTGACAGTGTGAGC 60
              ||||.|||||||||||||||||||||| || ||||||||||||||||||| |||||||||
Db          1 ATGGAATCCACAGGGCCAGGTTCTTATGTTACTCTGCTATGGGTATCTGGAACCTGTGGG 60

Qy         61 GACATTGTGCTGACTCAGTCTCCAGACTCCCTGGCTGTGTCTCTAGGCGAGAGGGCCACT 120
              ||||||||| || |||||||||||    ||||| ||||      | ||||||| ||  |||
Db         61 GACATTGTGATGTCACTCTCCTCATCCTTCTCTACCGTCGTCCACATCGGAGTCAGAATGTCTTACT 120

Qy        121 ATTAACTGCAAATCCAGTCAGACTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTT 180
              || |||||||  |||||||||| || |  | ||||| |  | | ||| |||||||
Db        121 ATCAACTGCAAGTCCAGTCAGAGTCTTTTATACAGCTCCAATAAAAGAATTACTTGGCC 180

Qy        181 TACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTTATCTACTGGGCATCTACTCGGGAA 240
              |||||||||||||||||||||| |||||||||||||| ||||||||||| ||||||
Db        181 TACTACAGAAACCAGGGACAGCCTCCTAAAGTGCTTATTTACTGGGCATCTACCCGGGAA 240

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
              | |||||||| |||||||||| ||| |||| |||| |||||||||| |||||||||||
Db        241 TAATCTCGTGTCCCTTATCGCTTCTCTGGCAGTGGGTCTGGGACTGATTTCACTCTCACC 300

Qy        301 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATAATAATTATCCTTAT 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATAATAATTATCCTTAT 360

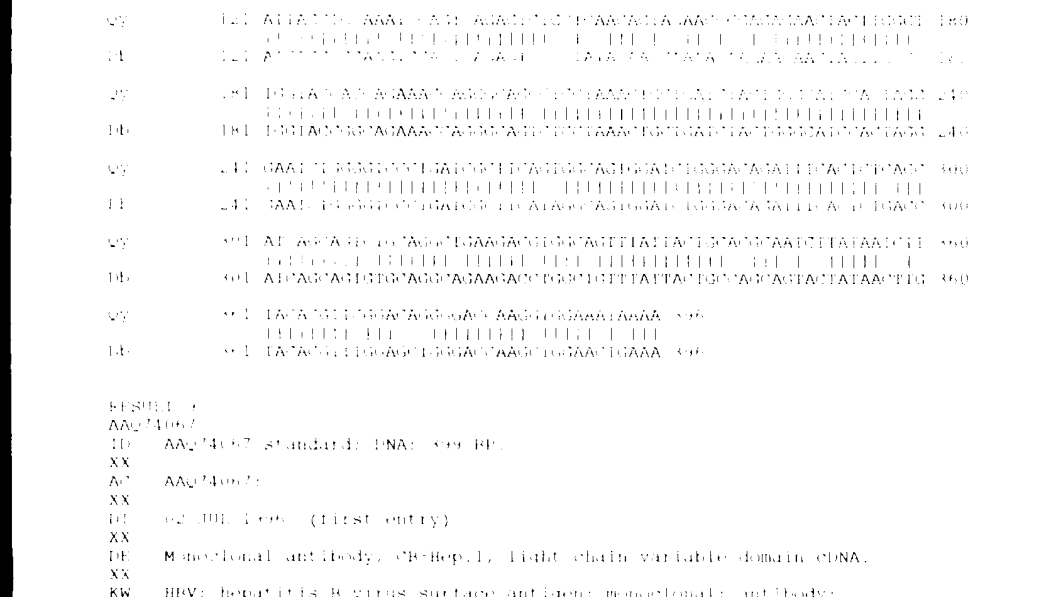
Qy        361 CCTCTTACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 398
              |  ||||||||||  ||||||||||||||||||||||||
Db        361 ACTTTTGGTTCGGGGGGACCAAGCTGGAAATAAAA 398


RESULT 2
AA143415
ID   AA143415 standard; cDNA to mRNA; 402 BP.
XX
AC   AA143415;
XX
DT   17-FEB-1997  (first entry)
XX
DE   Xenograft antibody HAR 1 light chain variable region cDNA.
XX
KW   Xenograft rejection; xenotransplantation; organ transplant;
KW   animal model; hamster; monoclonal antibody; HAR 1; ds.
XX
OS   Mathus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..402
FT                   /*tag= a
FT                   /product= "immunoglobulin variable region"
FT                   /standard_name= "HAR 1 kappa light chain variable region"
FT                   /label= VK Region
FT                   /note= "HAR 1 kappa light chain variable region"
FT   misc_RNA        1..60
FT                   /*tag= b
FT                   /standard_name= "Leader"
FT                   /label= Leader
FT   misc_RNA        61..342
FT                   /*tag= c
FT                   /standard_name= "Framework region 1"
FT                   /label= FR 1
FT                   /note= "framework region 1 of HAR 1 kappa light
FT                   chain variable region"
FT   misc_RNA        343..366
FT                   /*tag= d
FT                   /standard_name= "CDR 1"
FT                   /label= CDR 1
FT                   /note= "complementarity determining region 1 of
FT                   HAR 1 kappa light chain variable region"
FT   misc_RNA        367..525
FT                   /*tag= e
FT                   /standard_name= "Framework region 2"
FT                   /label= FR 2
FT                   /note= "framework region 2 of HAR 1 kappa light
FT                   chain variable region"
FT   misc_RNA        526..546
FT                   /*tag= f
FT                   /standard_name= "CDR 2"
FT                   /label= CDR 2
FT                   /note= "complementarity determining region 2 of
FT                   HAR 1 kappa light chain variable region"
FT   misc_RNA        547..642
FT                   /*tag= g
FT                   /standard_name= "Framewrok region 3"
FT                   /label= FR 3
FT                   /note= "framework region 3 of HAR 1 kappa light
FT                   chain variable region"
FT   misc_RNA        643..666
FT                   /*tag= h
FT                   /standard_name= "CDR 3"
FT                   /label= CDR 3
FT                   /note= "complementarity determining region 3 of
FT                   HAR 1 kappa light chain variable region"
FT   misc_RNA        667..402
FT                   /*tag= i
FT                   /standard_name= "Framework region 4"
FT                   /label= FR 4
FT                   /note= "framework region 4 of HAR 1 kappa light
FT                   chain variable region"
XX
PN   WO9636358-A1.
XX
PD   21-NOV-1996.
XX
PF   14-MAY-1996;   96WO-US06804.
XX
PR   15-MAY-1995;   95US-0440621.
XX
PA   (CEDA ) CEDARS SINAI MEDICAL CENT.
XX
PI   Cramer DV;  Makowka L;  Wu G;
XX
DR   WPI; 1997-011852/01.
DR   P-PSDB; AAW06206.
XX
PT   Inhibiting xenograft rejection by modifying antigen expression of
PT   the graft - prevents binding of anti-donor antibody and prolongs
PT   graft survival
XX
PS   Claim 10; Page 99; 135pp; English.
XX
CC   A cDNA clone (AA143415) codes for the kappa light chain variable
CC   region (AAW06206) of the HAR rat anti hamster xenograft monoclonal
CC   antibody HAR 1.  It was obtd. from a HAR-1 light chain cDNA library
CC   by PCR amplification (see also AA143425-26) and can be used to
CC   produce recombinant HAR 1 antibody fragments, e.g. F(ab')2 and
CC   Fab'.  These block binding of preformed anti-donor xenograft
CC   antibodies in a recipient animal serum to antigen expressed by
CC   endothelial cells of the xenograft, i.e. they inhibit antibody
CC   mediated rejection, thereby prolonging the survival of the hamster
CC   xenograft in a recipient.
XX
SQ   Sequence 402 BP; 102 A; 99 C; 107 G; 94 T; 0 other;

  Query Match             71.1%;  Score 293.6;  DB 18;  Length 402;
  Best Local Similarity   83.8%;  Pred. No. 9.6e-86;
  Matches  332;  Conservative    0;  Mismatches   64;  Indels    3;  Gaps    0;

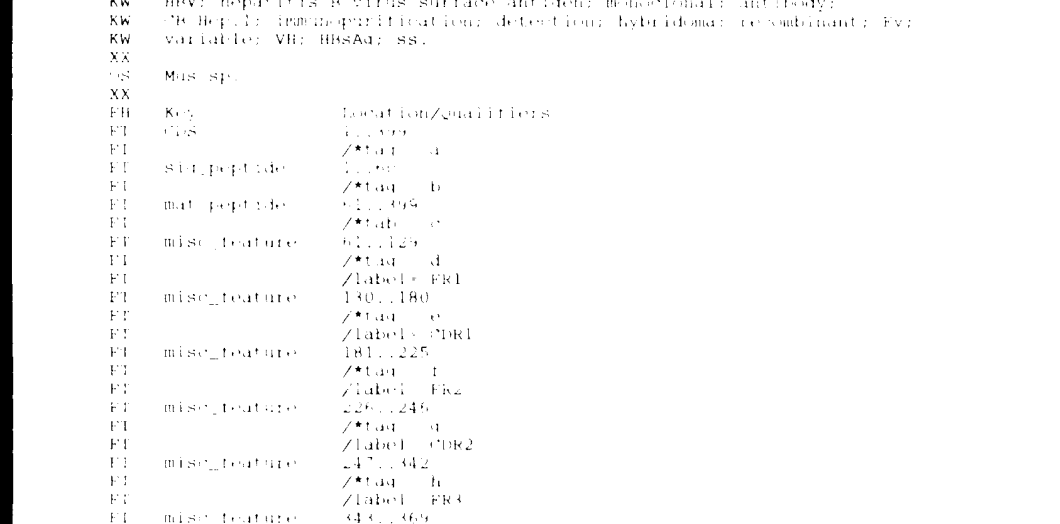
Qy          1 ATGGAGACCACAGGCCAGGTTCTTATGTTACTCTGCTATGGGTATCTGGAACCTGTGGG 60
              |||| |||||| | ||||| || || |  |||||||| ||||||||||| ||||||||
Db          1 ATGGAATCCACAGGGCCAGGTTCTTATGTTACTCTGCTATGGGTATCTGGAACCTGTGGG 60

Qy         61 GACATTGTGCTGACTCAGTCTCCAGATTCCCTGGCTGTGTCTCTAGGCGAGAGGGCCACT 120
              ||||||||| |||| ||| |||||   |||| ||||||      ||| |||| || ||||
Db         61 GACATTGTGATGTCACTCTCCTCATCCTTCTCTACCGTCGTCCACATCGGAGTCAGAATGTCTTACT 120
```



RESULT 9
AAQ74067
ID AAQ74067 standard; DNA; 999 BP.
XX
AC AAQ74067;
XX
DT 02-JUL-1999 (first entry)
XX
DE Monoclonal antibody, cBcHep.1, light chain variable domain cDNA.
XX
KW HBV; hepatitis B virus surface antigen; monoclonal antibody;
KW cBcHep.1; immunopurification; detection; hybridoma; recombinant; Fv;
KW variable; VH; HBsAg; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..999
FT /*tag= a
FT sig_peptide 1..60
FT /*tag= b
FT mat_peptide 61..399
FT /*tag= c
FT misc_feature 61..129
FT /*tag= d
FT /label= FR1
FT misc_feature 130..180
FT /*tag= e
FT /label= CDR1
FT misc_feature 181..225
FT /*tag= f
FT /label= FR2
FT misc_feature 226..246
FT /*tag= g
FT /label= CDR2
FT misc_feature 247..342
FT /*tag= h
FT /label= FR3
FT misc_feature 343..369
FT /*tag= i
FT /label= CDR3
FT misc_feature 370..399
FT /*tag= j
FT /label= FR4
XX
PN EP0866696-A1.
XX
PD 14-DEC-1995.
XX
PF 29-JUN-1995; 95EP-0201758.
XX
PR 29-JUN-1994; 94GB-0013074.

XX
PA (INSU-) INST NAT SANTE & RECH MEDICALE.
PA (SOMS-) SOMERE E M.
XX
PI Ayala Avila MA, Zamora Baeza FJM, del Carmen Dominguez Gerita M;
PI Fernandez de Cossio Borta-Duque ME, Castellanos Cowley LVG;
XX
DR WPI; 1996-021914/03.
DR P-PSDB; AAB80909.
XX
PT New recombinant single chain FV antibody fragment useful for
PT immunopurification, and detection of HBsAg
XX
PS Claim 1; Page 19; 23pp; English.
XX
CC AAQ74056 and AAQ74067 encode the heavy and light chain variable domains
CC of the murine hybridoma-derived monoclonal antibody cBcHep1 Fv region.
CC The heavy and light chain regions are used to produce a recombinant
CC antibody fragment having specificity for the hepatitis B virus
CC surface antigen (HBsAg). The recombinant antibody may be used for
CC immunopurification of HBsAg, in immunoassays for the detection of
CC HBsAg and for insolubilisation of heterologous fusion proteins
CC expressed in E. coli aiding their purification.
XX
SQ Sequence 999 BP; 98 A; 88 C; 101 G; 112 T; 0 other;



RESULT 10
AAI60734
ID AAI60734 standard; cDNA; 449 BP.
XX
AC AAI60734;
XX
DT 25-SEP-1997 (first entry)
XX
DE cDNA encoding wild type murine anti-E selectin antibody CY1087V(1).
XX
KW Humanised; murine; mouse; E selectin; antibody; light chain;
KW variable region; detection; inhibition; mediation; cell adhesion;
KW diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
KW acute respiratory distress syndrome; stress cystic breast disease;

```
KW   cancer; treatment; splanchnic occlusion shock; psoriasis;
KW   complement; 43.
XX
OS   Mus spp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..426
FT                   /*tag= a
FT                   /note= "no stop codon, sized"
XX
PN   W09640942-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;    96WO-SE000294.
XX
PR   07-JUN-1995;    95US-0482112.
XX
PA   (CYTE ) CYTEL CORP.
XX
PI   Bendig MM, Jones PT, Perez C, Saldanha JW, Williams MA;
PI   Jones S;
XX
DR   WPI; 1997-027172/25.
DR   P-PSDB; AAW19454.
XX
PT   Humanised anti-E-selectin antibody - useful for diagnosis and
PT   treatment of, e.g. inflammatory responses, septic shock, acute
PT   respiratory distress syndrome or cancer
XX
PS   Example 11; Page 56; 80pp; English.
XX
CC   The present sequence encodes the wild type murine anti-E-selectin
CC   antibody (Ab) light chain variable region, CY1787V(L), which was
CC   used in the preparation of the humanised anti-E-selectin Ab light
CC   chain variable regions, CY1788V(LA-B). The humanised Ab can
CC   be used to detect E-selectin, or inhibit E-selectin mediated cell
CC   adhesion. They can also be used to diagnose, reduce or inhibit an
CC   inflammatory response, or the severity of pathologies, e.g. septic
CC   shock, acute respiratory distress syndrome, wound associated
CC   sepsis, cystic breast disease or cancer, or treat, e.g.
CC   splanchnic occlusion shock, or psoriasis. They can be administered
CC   to a human without inducing an immune response. In addition, the
CC   effector portion of the Ab can interact with various components of
CC   the human immune system, including complement.
XX
SQ   Sequence 426 BP; 108 A; 110 C; 116 G; 105 T; 0 other;

  Query Match             72.4%;  Score 286.8;  DB 17;  Length 426;
  Best Local Similarity   84.5%;  Pred. No. 4.6e-84;
  Matches  333;  Conservative    0;  Mismatches   61;  Indels    6;  Gaps    1;

Qy          1 ATGGATTTACAGGTGCAGGTTCTTATAGTGTCTTTGTTTCTGGCTGGTACCTTGTGGAG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 ATGGATTTACAGGTGCAGGTTCTTATAGTGTCTTTGTTTCTGGCTGGTACCTTGTGGAG 267

Qy         61 GATATTGTGATGACACAGTCTCCAGACTCCCTAGCTGTGTCTCTAGGCGAGAGGGCCACC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GATATTGTGATGACACAGTCTCCAGACTCCCTAGCTGTGTCTCTAGGCGAGAGGGCCACC 327

Qy        121 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 387

Qy        181 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 447

Qy        241 GAATCCGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 GAATCCGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 507

Qy        301 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 567

Qy        361 CCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 399
              |||||||||||||||||||||||||||||||||||||||
Db        568 CCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 606

RESULT 11
AAI34152
ID   AAI34152 standard; DNA; 418 BP.
XX
AC   AAI34152;
XX
DT   14-FEB-1997  (first entry)
XX
DE   Monoclonal antibody PAI-3F10 variable light chain encoding DNA.
XX
KW   PAI-3F10; antibody; hybridoma; LMBP1322CB; cancer; target; epitope;
KW   breast, colorectal, lung, ovary, dysplasia, neoplasia, ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..418
FT                   /*tag= a
FT                   /note= "no start or stop codon"
XX
PN   W09622310-A1.
XX
PD   25-JUL-1996.
XX
PF   15-JAN-1996;    96WO-SE000029.
XX
PR   18-JAN-1995;    95SE-0000148.
XX
PA   (BIOI-) BIOINVENT INT AB.
XX
PI   Carlsson R, Jansson B;
XX
DR   WPI; 1996-354478/35.
DR   P-PSDB; AAB90459.
XX
PT   Monoclonal antibody PAI-3F10 produced by hybridoma BCCM LMBP1322CB
PT   useful to target cancer cells for killing or detection
XX
PS   Claim 10; Fig 10; 62pp; English.
XX
CC   AAI34152 encodes the variable light (VL) chain of monoclonal antibody
CC   PAI-3F10 produced by hybridoma BCCM LMBP1322CB. The antibody is
CC   directed against an epitope present on cancer cells, in particular
CC   breast, ovary, lung and colorectal cancer cells. The antibody is
CC   useful for detecting cancer cell epitopes and hence in the diagnosis
CC   of cancer. The antibody can be conjugated to a cytotoxic compound and
CC   targetted to cancer cells to kill them.
XX
SQ   Sequence 418 BP; 102 A; 100 C; 107 G; 109 T; 0 other;

  Query Match             72.4%;  Score 286.8;  DB 17;  Length 418;
  Best Local Similarity   84.8%;  Pred. No. 4.6e-83;
  Matches  333;  Conservative    0;  Mismatches   57;  Indels    5;  Gaps    1;

Qy          1 ATGGATTTACAGGTGCAGGTTCTTATAGTGTCTTTGTTTCTGGCTGGTACCTTGTGGAG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGATTTACAGGTGCAGGTTCTTATAGTGTCTTTGTTTCTGGCTGGTACCTTGTGGAG 60

Qy         61 GATATTGTGATGACACAGTCTCCAGACTCCCTAGCTGTGTCTCTAGGCGAGAGGGCCACC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATATTGTGATGACACAGTCTCCAGACTCCCTAGCTGTGTCTCTAGGCGAGAGGGCCACC 120

Qy        121 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 180

Qy        181 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 240

Qy        241 GAATCCGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATCCGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300

Qy        301 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 360

Qy        361 CCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 399
              |||||||||||||||||||||||||||||||||||||||
Db        361 CCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA 399
```

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Qy        186 CCAGCAGAAACCAGGGCAGCCAGGCAAACTCCTAATCTACTTGGCATCTACCCTGGAATC 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGCAGAAACCAGGGCAGTCCCTAAACTGCTGATTTACTTGGCATCTACCCTGGAATC 240

Qy        246 TGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAG 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAG 300

Qy        306 CAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATGGCTATCCTCG 365
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGTCTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATGGCTATCCTCG 360

Qy        366 CAGGTTCGGACAGGGGACCAAGGTGGAAATAAAA 399
              |||||||||||||||||||||||||||||||||||
Db        361 CAGGTTCGGACAGGGGACCAAGGTGGAAATAAAA 394


RESULT 12
AAI72240
ID   AAI72240 standard; cDNA; 439 BP.
XX
AC   AAI72240;
XX
DT   03-JAN-1998  (first entry)
XX
DE   Chimeric MAb 15 PCR modified light chain variable region cDNA.
XX
KW   Humanised antibody; monoclonal antibody; MAb 15; tumour;
KW   lung cancer; therapy; ds.
XX
OS   Chimeric Mus musculus.
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     1..57
FT                   /*tag= a
FT   mat_peptide     58..429
FT                   /*tag= b
XX
PN   EP781847-A1.
XX
PD   02-JUL-1997.
XX
PF   25-OCT-1996;    96EP-0117154.
XX
PR   06-NOV-1995;    95EP-0117407.
XX
PA   (MEFF ) MERCK PATENT GMBH.
XX
PI   Bendig M.  Jones T.  Saldana J;
XX
DR   WPI; 1997-344764/31.
DR   P-PSDB; AAW21655.
XX
PT   Humanised form of murine monoclonal antibody MAb 15 useful for
PT   treating lung cancer
XX
PS   Disclosure; Fig 4; 71pp; English.
XX
CC   This cDNA sequence comprises the light chain variable region, VL
CC   sequence of murine monoclonal antibody (MAb) 15 (U.S.M.A.C.2117),
CC   modified for the expression of chimeric 15 antibody. The 5' and
CC   3' ends of the VL sequence (see also AAI72238) were modified by
CC   PCR (see AAI72243-44) to provide a Kozak sequence for efficient
CC   translation, a 5' HindIII site for cloning into HCMV vectors, a
CC   3' splice donor site at the J-C junction for splicing the mouse
CC   variable regions to human constant regions and a 3' BamHI site for
CC   cloning into HCMV vectors. The VH sequence was similarly modified
CC   (see AAI72239). The modified VL and VH sequences were used in a
CC   claimed process to model and design novel humanised, reshaped MAb
CC   15 having humanised, reshaped VL and VH sequences (see AAW21651 and
CC   AAW21652), which can be used for treating tumours, especially lung
CC   cancer, and for the manufacture of a drug related to tumours,
CC   especially lung cancer.
XX
SQ   Sequence 439 BP; 109 A; 107 C; 122 G; 101 T; 0 other;

  Query Match          72.1%;  Score 285.4;  DB 18;  Length 439;
  Best Local Similarity   84.0%;  Pred. No. 4.8e-83;
  Matches  336;  Conservative    0;  Mismatches   61;  Indels    8;  Gaps    1;

Qy          1 ATGGATTTTCAGGGCCAGATTCTTTATATTAGTCTGCTGCTATGGGTATCTGGCACCTGTGGG 60
              ||||| |||||| | | |||||||| || ||||||||||||||||||| |||||||
Db         28 ATGGAGTCACAGACCCAGGTCCTCATATGTTACTGCTGCTATGGGTATGTGGTACCCTGTGGG 87

Qy         61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCCTTAGGGAGAGGGCCACT 120
              |||||||||| || |||||||||||    |||| ||||      | |||||| | |||
Db         88 GACATTGTGATGTCACAGTCT-CATCCTCCCTACCTGTGCAGTCTGGAGAGAAAGTTACT 146

Qy        121 ATTAGCTGCAAATCCAGTCAGAGTCTCCTAAACAGTAGAACCCGAGAGAACTACTTGGCT 180
              || |||||||| |||||||||| ||  |  | |||| |  | | |||||||||||||
Db        147 ATGAGCGAAATCCAGTATAGACTTTTATATAGCAGCAACCAAAAGAACTACTTAGCT 207

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCAGGCAAACTCCTAATCTACTTGGCATCTACCCTGGAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 TGGTACCAGCAGAAACCAGGGCAGTCCCTAAACTGCTGATTTACTTGGCATCTACCCTGGAATC 267

Qy        241 CAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCA 327

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATA   AT 357
              ||||||||  || || ||||||||||  |||||||||||||||||||||||   || || || ||  ||
Db        328 ATCAACAGCGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATGGCTAT 387

Qy        358 CCTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
              || |  ||||||||  || |||||| ||||||| |||
Db        388 CCTCCTACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 426


RESULT 13
AAI72238
ID   AAI72238 standard; cDNA; 460 BP.
XX
AC   AAI72238;
XX
DT   03-JAN-1998  (first entry)
XX
DE   Mouse MAb 15 light chain variable region cDNA.
XX
KW   Humanised antibody; monoclonal antibody; MAb 15; tumour;
KW   lung cancer; therapy; ds.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     1..72
FT                   /*tag= a
FT   mat_peptide     73..411
FT                   /*tag= b
XX
PN   EP781847-A1.
XX
PD   02-JUL-1997.
XX
PF   25-OCT-1996;    96EP-0117154.
XX
PR   06-NOV-1995;    95EP-0117407.
XX
PA   (MEFF ) MERCK PATENT GMBH.
XX
PI   Bendig M.  Jones T.  Saldana J;
XX
DR   WPI; 1997-344764/31.
DR   P-PSDB; AAW21653.
```

```
XX
RT   Humanised form of murine monoclonal antibody MAb 15 useful for
RT   treating lung cancer
XX
RL   Claim 11; Fig 1; 72pp; English.
XX
CC   This cDNA sequence encodes the light chain variable region VL
CC   (AAW21654) of murine monoclonal antibody (MAb) 15 (DSM ACC2117),
CC   a MAb that shows a therapeutic effect on human tumour cells,
CC   especially human lung cancer. The clone was isolated from
CC   hybridoma cDNA using a degenerate leader sequence primer (AAI72239)
CC   and a kappa constant region reverse primer (AAI72240). The VH region
CC   (see AAI72267) was also amplified. The VL and VH sequences were
CC   used in a claimed process for the production of novel humanised,
CC   reshaped MAb 15 having humanised, reshaped VL and VH sequences
CC   (see AAW21653 and AAW21652), which can be used for treating tumours,
CC   especially lung cancer, and for the manufacture of a drug related
CC   to tumours, especially lung cancer.
XX
SQ   Sequence 460 BP; 112 A; 118 C; 113 G; 117 T; 0 other;

  Query Match          72.1%;  Score 285.4;  DB 18;  Length 460;
  Best Local Similarity   84.0%;  Prod. No. 4.2e-85;
  Matches  336;  Conservative    0;  Mismatches   61;  Indels    4;  Gaps    1;

Qy          1 ATGGATTTACAGGCGCAGATTCTTATATTCGTCGCTATGGTATCTGTGACCTTGGGG 60
              ||||| |||||  ||| |||||||||| || ||||||||||||||||||||| ||||||||
Db        13 ATGGAGTCACATTCCCTGGTTCTTATGTTACTCTCTATGGGTATCTGTTACCTGTGGG 72

Qy         61 AACATTGTGATGACACAGTCTCCAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGC 120
              |||||||| || |||||||||||   |||| ||||     | |||||| || |||
Db         73 AACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTTACT 132

Qy        121 ATTAGCTGCAAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180
              | |||||| | |||||||||| || |  | | |||| |  | | ||||||||||||||
Db        133 ATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTAGCAATCAAAAGAACTACTTGGCC 192

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              ||||||||||| ||||||||||| ||| |||||||||| ||||||||||||||||||||
Db        193 TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAGTGCTGATTTACTGGGCATCCACTAGG 252

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGAACAGATTTCACTCTCACC 300
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GAATCTGGAGTCCCTGATCGCTTCATAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 312

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGGCAATCTTATAATCTT 360
              |||||||| |||||||||||||| ||||||||||||||||||||| |||||||||||||.
Db        313 ATCAGCAGTCTGGAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATCTTATAATCTC 372

Qy        361 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
              |||||||    || ||||| |||||.| |||
Db        373 TACATTTCGGAGGGGGACCAAGCTGGAAATCAAA 408


RESULT 14
AAX44405
ID   AAX44405 standard; cDNA; 442 BP.
XX
AC   AAX44405;
XX
DT   25-JUN-1999  (first entry)
XX
DE   Mouse MAb 6A4 light chain variable region encoding DNA.
XX
KW   Rolling templates; nucleic acid synthesis; polynucleotide polymerase;
KW   gene product; primer; monoclonal antibody; 6A4; ss.
XX
OS   Mus sp.
XX
PN   WO9944063-A1.
XX
PD   25-MAR-1999
XX
PF   15-SEP-1998;  98WO-US19157.
XX
PR   15-SEP-1997;  97US-0928856.
XX
PA   (BIAT/) BIATT A F.
PA   (ROSE/) ROSE F D.
XX
PI   Biatt AC, Rose FD;
XX
DR   WPI; 1999-244045/20.
DR   P-PSDB; AAT06859.
XX
PT   Producing specific polynucleotides using rolling templates
XX
PS   Example 6; Page 40; 109pp; English.
XX
CC   The invention relates to a method for producing polynucleotides having a
CC   defined sequence using rolling templates that successively add
CC   nucleotides (nts) to a longer primer strand. The method comprises: (i)
CC   incubating, under annealing conditions, a primer and a template that has
CC   a 5' region not complementary to the primer, a 3'-region complementary to
CC   the 3' end of primer and a non-reactive 3' terminus, with the template
CC   being shorter than the primer; (ii) reacting the primer with at least one
CC   nt in presence of a template-dependent polynucleotide polymerase to
CC   extend it by at least one nt (complementary to the 5'-region of template)
CC   at its 3'-end; (iii) separating the template and the extended primer; and
CC   (iv) repeating the cycle of (i) (iii) as often as needed to synthesize
CC   the desired polynucleotide. The method is especially used to produce
CC   genes or their segments. The method provides fast, accurate, inexpensive
CC   synthesis of RNA or DNA and is more efficient than chemical coupling
CC   processes. It has higher specificity and eliminates the need for
CC   deprotection. The products can be cloned directly. The method avoids
CC   problems of waste disposal and includes an inherent editing effect
CC   (failure sequences will not be extended further in subsequent rounds) so
CC   that purification of the end product is facilitated. Synthesis may take
CC   place on a vector, simplifying cloning and sequences with codon usage
CC   optimized for a particular host can be prepared. This represents the
CC   nucleotide sequence of the light chain variable region of the mouse
CC   monoclonal antibody (MAb) 6A4, synthesised by the method of the
CC   invention.
XX
SQ   Sequence 442 BP; 88 A; 87 C; 87 G; 80 T; 0 other;

  Query Match          [illegible]%;  Score 280.2;  DB 20;  Length 442;
  Best Local Similarity   90.2%;  Prod. No. 2.3e-82;
  Matches  [illegible];  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          61 AACATTGTGATGACACAGTCTCCAGCATTCATGTCCACATCAGTAGGAGACAGGGTCAGC 120
              |||||||| || |||||||||||   |||||||||     |||||||| || |||
Db          1 GACATTGTGATGTCACAGCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACT 60

Qy         121 ATTAGCTGCAAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180
              || |||||||||||||||||||||||||||||||||||| |||||| |||||| ||||||
Db         61 ATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAATAACCCGAAAGAACTACTTGTCT 120

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGAACAGATTTCACTCTCACC 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGGCAATCTTATAATCTT 360
               |||||||| |||||||||||||| |||||||||||||||||||| |||||||||||||.
Db         241 ATCAGCAGTCTGGAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATCTTATAATCTC 300

Qy         361 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
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Db         301 TACATTTCGGAGGGGGACCAAGCTGGAAATCAAA 336


RESULT 15
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AAQ62958
ID   AAQ62958 standard; DNA; 1443 BP.
XX
AC   AAQ62958;
XX
DT   04-SEP-1994  (first entry)
XX
DE   Glycophorin antibody b38 Fab coding region.
XX
KW   Glycophorin; antibody b38; target binding polypeptide; PCR;
KW   polymerase chain reaction; primer; antibody engineering;
KW   humanized antibody; phagemid pHFA; plasmid p569;ss.
XX
OS   Synthetic.
XX
PN   WO9404721-A.
XX
PD   24-FEB-1994.
XX
PF   24-SEP-1993;   93WO-AU00491.
XX
PR   25-SEP-1992;   92AU-0004978.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Atwell JL;  Colman PM;  Hudson PJ;  Irving RA;  Kortt A;
PI   Lah M;  Mallyri;  Power BE;
XX
DR   WPI; 1994-135515/16.
XX
PT   New target-binding polypeptide(s) used for diagnosis, etc. -
PT   having a stable core polypeptide region with at least one
PT   target-binding region covalently attached, opt. mutated to alter
PT   specificity, etc.
XX
PS   Disclosure; Page 42; 67pp; English.
XX
CC   PCR primers given in AAQ62951-52 were used to clone anti-glycophorin
CC   antibody b38 Fab coding region.  The DNA sequence of the first 1443
CC   bases of the Fab fragment in pHFA, ready for ligation post PCR
CC   amplification for ligation into p569, is given in AAQ62958.
XX
SQ   Sequence 1443 BP; 391 A; 388 C; 351 G; 313 T; 0 other;

  Query Match          70.7%;  Score 279.8;  DB 15;  Length 1443;
  Best Local Similarity   84.6%;  Pred. No. 5.2e-81;
  Matches  814;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          25 TATTACTGCTGTATGGTATCTGGCACTGTGGGGACATTGTGCTGACACAGTCTCCAG 84
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Db         734 TCTTACCGTTACTGTTTACCCCGGTAACCAAAGCCGACATCGTCATGTCACAGTCTCCAT 793

Qy          85 ATCCCCTGGCTGTAAGCTTACGAGAGAGGGCCACTATTAGCTGCAAATCCAGTCAGAGTC 144
                 ||||||||||     |||||||| || |||||| ||||||| ||||||||||||||
Db         794 CCTCCCTGGCTGTGTCAGTAGGAGAGAAGGTCACTATGAGCTGCAGATCCAGTCAGAGTC 853

Qy         145 TGCTCAACAGTAGAACCCGAGAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGC 204
               || ||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||
Db         854 TGTTCAACAGTAGAACCCGAAAGAACTACTTGACTTGGTACCAGCAGAAACCAGGGCAGT 913

Qy         205 CTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCA 264
               |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         914 CTCCTAAACCGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCA 973

Qy         265 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGGCTGAAGACG 324
               ||||||||||||.|||||||||||||||||||||||||||||| ||||||||||||||
Db         974 CAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGGCTGAAGACG 1033

Qy         325 TGGCAGTTTATTACTGCACGCAATCTATAATCTTTACACGTTCGGACAGGGGACCAAGC 384
               |||||| |||||||||| ||||||||||||||    |||||||    || ||||||
Db        1034 TGGCAGATTATTACTGCAAGCAATCTTATAATCTTCCGTTCGGTCAGGGCACCAAGC 1093

Qy         385 TGGAAATAAAA 396
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Db        1094 TGGAAATTAAA 1104


Search completed: June 17, 2003, 19:24:44
Job time : 150.667 secs
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SeqSite Version 5.1.1
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SW nucleic - nucleic search, using sw model

Run on: June 17, 2003, 19:24:50 ; Search time 13.82 Seconds
(without alignments)
5523.418 Million cell updates/sec

Title: US-09-249-011B-7
Perfect score: 396
Sequence: 1 atggattcacaaacccaagt.....ggacctaaattttttaataaaa 396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US09_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09A_NEW_1.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US10_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	396	100.0	396	9	US-09-249-011A-7	Sequence 7, Appli
2	392.8	99.2	1960	9	US-09-249-011A-21	Sequence 21, Appl
3	360.8	91.1	396	9	US-09-249-011A-3	Sequence 3, Appli
4	255	64.4	1033	10	US-09-799-514-2	Sequence 2, Appli
5	254.6	64.0	463	9	US-09-925-299-453	Sequence 453, App
6	253.6	64.0	463	10	US-09-925-299-453	Sequence 453, App
7	252	63.6	788	9	US-10-158-646-58	Sequence 58, Appl
8	246.4	62.2	390	9	US-10-146-305-5	Sequence 5, Appli
9	244.8	61.8	336	9	US-09-056-052-17	Sequence 17, Appl
10	244	61.6	389	9	US-09-995-529-1	Sequence 1, Appli
11	243.4	61.5	336	9	US-10-056-052-9	Sequence 9, Appli
12	242.6	61.3	9611	9	US-09-897-511A-34	Sequence 34, Appl
13	240.6	60.8	9611	10	US-09-897-006-34	Sequence 34, Appl
14	240	60.6	347	10	US-09-897-511-8	Sequence 8, Appli
15	240.2	60.7	336	9	US-10-056-052-13	Sequence 13, Appl
16	238.8	60.3	384	10	US-09-905-243-54	Sequence 54, Appl
17	232.8	58.8	924	10	US-09-742-693-26	Sequence 26, Appl
18	232.6	58.7	336	9	US-10-056-052-5	Sequence 5, Appli
19	232.6	58.7	949	10	US-09-742-693-25	Sequence 25, Appl
20	231.2	58.4	3344	9	US-10-176-966-17	Sequence 17, Appl
21	229.6	57.7	339	9	US-10-121-464-5	Sequence 5, Appli
22	227.4	57.4	764	10	US-09-978-752-13	Sequence 13, Appl
23	227	57.3	339	9	US-10-121-464-1	Sequence 1, Appli
24	226.4	57.2	4661	9	US-09-897-511A-10	Sequence 10, Appl
25	226.4	57.2	4661	10	US-09-897-006-10	Sequence 10, Appl
26	225.4	56.9	327	10	US-09-828-708-112	Sequence 112, Appl
27	225.4	56.9	327	10	US-09-828-708-115	Sequence 115, Appl
28	225	56.8	759	10	US-09-978-752-10	Sequence 10, Appl
29	224.8	56.5	339	9	US-10-121-464-3	Sequence 3, Appli
30	220.6	55.7	342	10	US-09-274-163E-1	Sequence 1, Appli
31	220.6	55.7	723	10	US-09-791-578-5	Sequence 5, Appli
32	220.6	55.7	723	10	US-09-791-540-5	Sequence 5, Appli
33	220.6	55.7	758	9	US-09-956-086-1	Sequence 1, Appli
34	220.6	55.7	758	9	US-09-956-087-1	Sequence 1, Appli
35	220.6	55.7	782	9	US-09-985-442-1	Sequence 1, Appli
36	220.6	55.7	782	10	US-09-791-578-3	Sequence 3, Appli
37	220.6	55.7	782	10	US-09-791-540-3	Sequence 3, Appli
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39	220.6	55.7	818	9	US-09-985-442-3	Sequence 3, Appli
40	220.6	55.7	818	10	US-09-983-580-3	Sequence 3, Appli
41	219.2	55.4	339	9	US-09-894-849-1	Sequence 1, Appli
42	219.2	55.4	339	9	US-09-988-015A-1	Sequence 1, Appli
43	219.2	55.4	339	9	US-09-988-015A-22	Sequence 22, Appl
44	219.2	55.4	339	10	US-09-741-843-1	Sequence 1, Appl
45	219.2	55.4	339	10	US-09-978-752-9	Sequence 9, Appli

ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
AUTHORS
AUTHORS
AUTHORS
AUTHORS
AUTHORS
TITLE
JOURNAL
FEATURES
APPLICANT: O'BRIEN, DENISE
APPLICANT: RAO, RONITA
APPLICANT: VELDMAN, GEERTRUIDA M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
TITLE OF INVENTION: OF TREATMENT THEREWITH
FILE REFERENCE: 09702.0081-00000
CURRENT APPLICATION NUMBER: US/09/249,011A
CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 396
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Humanized
OTHER INFORMATION: murine anti-human B7-2 light chain
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(396)
US-09-249-011A-7

Query Match 100.0%; Score 396; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.2e-126;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATTCACAAACCCAAGTTCTCATATTTGTGTCTCTTGCTGTTTTTGTC 60
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Db 1 ATGGATTCACAAACCCAAGTTCTCATATTTGTGTCTCTTGCTGTTTTTGTC 60

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Qy          61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTATGGAGAGAGGGCCACT 120
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Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACCAGG 240
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Db         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATCTT 360

Qy         361 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
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Db         361 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396


RESULT 2
US-09-249-011A-21
; Sequence 21, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
;  APPLICANT: OH, MAN SUNG
;  APPLICANT:  VASQUEZ, MAXIMILIANO
;  APPLICANT:  CARRENO, BEATRIZ
;  APPLICANT:  CELNIKER, ABBIE CHERYL
;  APPLICANT:  COLLINS, MARY
;  APPLICANT:  GOLDMAN, SAMUEL
;  APPLICANT:  GRAY, GARY S.
;  APPLICANT:  KNIGHT, ANDREA
;  APPLICANT:  O'HARA, DENISE
;  APPLICANT:  RUP, BONITA
;  APPLICANT:  VELDMAN, GEERTRUIDA M.
;  TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
;  TITLE OF INVENTION:  OF TREATMENT THEREWITH
;  FILE REFERENCE: 0870.2/0081.00000
;  CURRENT APPLICATION NUMBER: US/09/249,011A
;  CURRENT FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;  LENGTH: 396
;  TYPE: DNA
;  ORGANISM: Mus sp.
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(396)
;  OTHER INFORMATION: Anti B7-2 light chain
US-09-249-011A-21

  Query Match             99.2%;  Score 392.8;  DB 9;  Length 1960;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-124;
  Matches  394;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           1 ATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGGTGAC 60
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Qy          61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTATGGAGAGAGGGCCACT 120
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Qy         121 ATTAGCTGCAAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180
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Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACCAGG 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         241 GAATCCGGGGTCCCTGATCGCTTCAGTGGCAGCGGATCTGGGACAGATTTCACTCTCACC 300
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Db        1612 GAATCCGGGGTCCCTGATCGCTTCAGTGGCAGCGGATCTGGGACAGATTTCACTCTCACC 1671

Qy         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATCTT 360
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Db        1672 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATCTT 1731

Qy         361 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
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RESULT 3
US-09-249-011A-3
; Sequence 3, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
;  APPLICANT: OH, MAN SUNG
;  APPLICANT:  VASQUEZ, MAXIMILIANO
;  APPLICANT:  CARRENO, BEATRIZ
;  APPLICANT:  CELNIKER, ABBIE CHERYL
;  APPLICANT:  COLLINS, MARY
;  APPLICANT:  GOLDMAN, SAMUEL
;  APPLICANT:  GRAY, GARY S.
;  APPLICANT:  KNIGHT, ANDREA
;  APPLICANT:  O'HARA, DENISE
;  APPLICANT:  RUP, BONITA
;  APPLICANT:  VELDMAN, GEERTRUIDA M.
;  TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
;  TITLE OF INVENTION:  OF TREATMENT THEREWITH
;  FILE REFERENCE: 0870.2/0081.00000
;  CURRENT APPLICATION NUMBER: US/09/249,011A
;  CURRENT FILING DATE:  1999-02-12
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;  LENGTH: 396
;  TYPE: DNA
;  ORGANISM: Murine sp.
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(396)
;  OTHER INFORMATION: Anti B7-2 light chain
US-09-249-011A-3

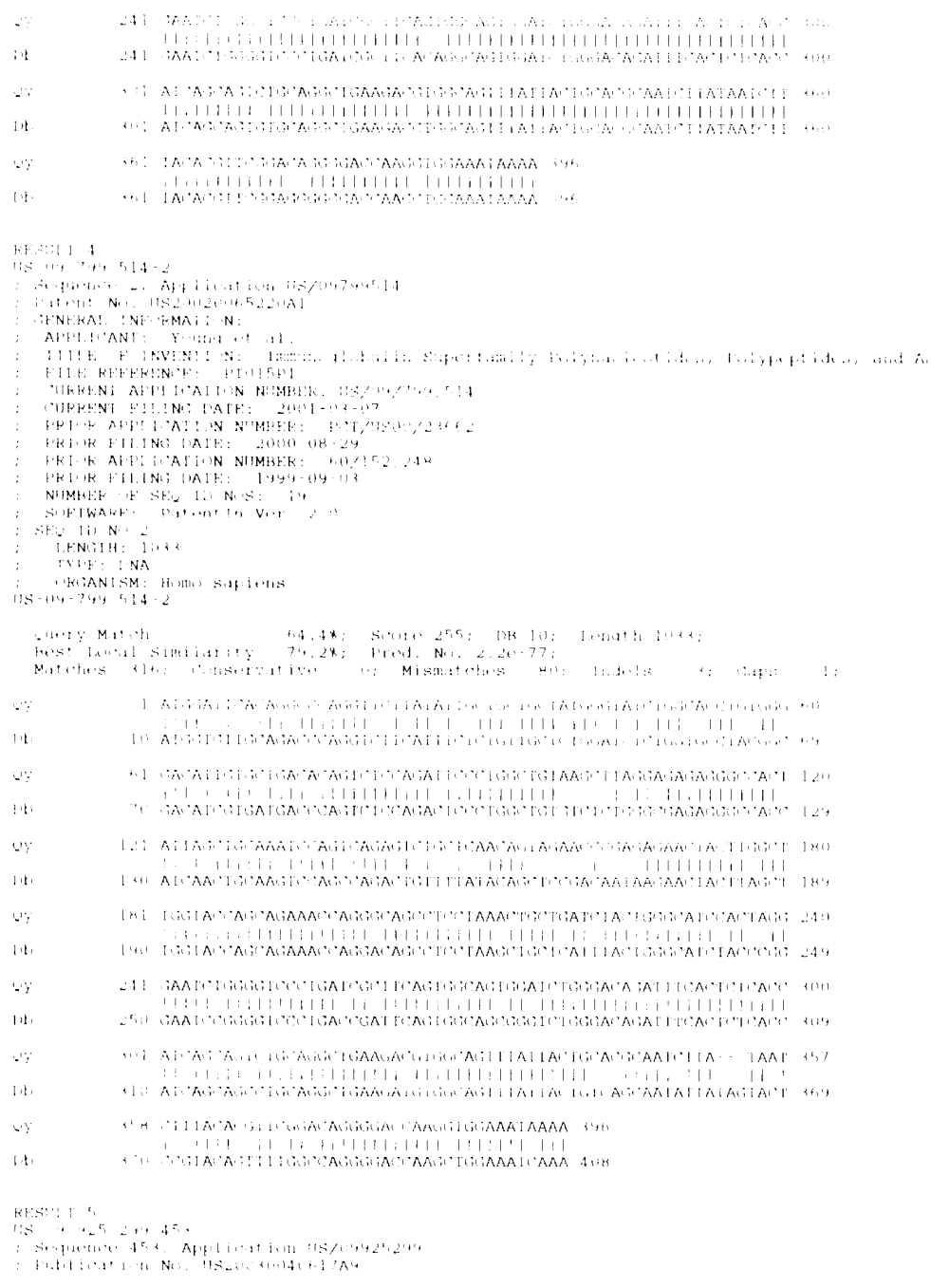
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  Best Local Similarity   94.4%;  Pred. No. 6.6e-114;
  Matches  374;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

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Qy          61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTATGGAGAGAGGGCCACT 120
               |||||||||||| |||||||||| |||||||||| |||||||||| |||||||| ||||||||
Db          61 GACATTGTGTTGTCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACT 120

Qy         121 ATTAGCTGCAAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180
               || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACCAGG 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCCACCAGG 240
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RESULT 4
US-09-299-514-2
; Sequence 2, Application US/09299514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Human Platelet Specifically Polynucleotides, Polypeptides, and A
; FILE REFERENCE: PI0159P1
; CURRENT APPLICATION NUMBER: US/09/299,514
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: PCT/US00/23662
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/152,249
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1033
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-299-514-2

Query Match 64.4%; Score 255; DB 10; Length 1033;
Best Local Similarity 79.2%; Pred. No. 2.2e-77;
Matches 316; Conservative 0; Mismatches 80; Indels 3; Gaps 1;

RESULT 5
US-09-925-299-453
; Sequence 453, Application US/09925299
; Publication No. US20030040017A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05083
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (315)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (356)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (404)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (426)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (435)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (453)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-453

Query Match 64.0%; Score 253.6; DB 9; Length 463;
Best Local Similarity 79.2%; Pred. No. 5e-77;
Matches 314; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

RESULT 6
US-09-925-299-453
; Sequence 453, Application US/09925299

; Patent No. US2002[illegible]
; GENERAL INFORMATION:
; APPLICANT: Regents of the
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: [illegible]
; CURRENT APPLICATION NUMBER: US/[illegible]
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: [illegible]
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/[illegible]
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1956
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (315)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (393)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (404)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (426)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (435)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-453

Query Match 64.0%; Score 253.6; DB 10; Length 464;
Best Local Similarity 78.7%; Pred. No. 5e-77;
Matches 314; Conservative 0; Mismatches 82; Indels 4; Gaps 1;

Qy 1 ATCGATTCACAGGCCAGGTCCTATATTGCTGCTGCTATGGTATCTGGACCTGTGGG 60
||||| | ||| ||||||| | || | ||| |||| ||| | |||| ||| |||
Db 7 ATGGTGTTGCAGACCCAGTCTTCATTTCTGTTGCTCTGGATCTGGTGCCTACGGG 66

Qy 61 GACATTGTGCTGACACAGTCTCCAGATCCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACT 120
|||| ||| |||| |||||||||| |||||||||| | || ||||||||||
Db 67 GACAGCCTCAAGAGCAGCTACTTGGCTTGGTACCAGCAGAAGCCAGGACAGCCT 126

Qy 121 ATTAACTGCAAATCCAGTCAGAGTCTTCTCAACAGCAACAATAAGAACTACTTAGCT 180
|| | |||||| |||| |||||| | | |||| || | |||| |||||||||| ||
Db 127 ATTAACTGGAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 186

Qy 181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
|||||||||||||||||||| |||||||||| |||| || |||||||| || ||
Db 187 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 246

Qy 241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
|||||||||||||||||||| || |||||||||| || |||||||||||||||||||
Db 247 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 306

Qy 301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATACTCT 360
|||||||| |||||||||||| |||||||||||||| |||| |||| | |
Db 307 ATCAGCAGCCTGCAGGCGGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 366

Qy 361 --- TACACCTTCGGCCAAGGGACCAAGCTGGAAATAAAA 396
||| ||||| |||||||||||| || |||
Db 367 CCTCGGCTGCACCTTCGGCCAAGGGACCAAGGTGGAGATCAAA 423

; Sequence 58, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K.W.
; APPLICANT: Sormasse, Thierry
; TITLE OF INVENTION: Assay Methods to Screen ANGER
; FILE REFERENCE: PA-0030 1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/294,249
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 58
; LENGTH: 788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: US20030073105A1 1101440.8
US-10-158-646-58

Query Match 63.6%; Score 252; DB 9; Length 788;
Best Local Similarity 78.6%; Pred. No. 2.2e-76;
Matches 316; Conservative 0; Mismatches 80; Indels 2; Gaps 1;

Qy 1 ATCGATTCACAGGCCAGGTCCTATATTGCTGCTGCTATGGTATCTGGACCTGTGGG 60
|||| | ||| ||||||| | || | ||| |||| ||| | |||| ||| |||
Db 22 ATGGTGTTGCAGACCCAGGTCTTCATTTCTGTTGCTCTGGATCTCTATGGTGCCTACGGG 81

Qy 61 GACATTGTGCTGACACAGTCTCCAGATCCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACT 120
|||| ||| |||| |||||||||| |||||||||| | || ||||||||||
Db 82 GACAGCCTCAAGAGCAGCTACTTGGCTTGGTACCAGCAGAAGCCAGGACAGCCTCCTAAC 141

Qy 121 ATTAACTGCAAATCCAGTCAGAGTCTTCTCAACAGCAACAATAAGAACTACTTAGCT 180
|| | |||||| |||| |||||| | | |||| || | |||| |||||||||| ||
Db 142 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 201

Qy 181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
|||||||||||||||||||| |||||||||| |||| || |||||||| || ||
Db 202 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 261

Qy 241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
|||||||||||||||||||| || |||||||||| || |||||||||||||||||||
Db 262 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 321

Qy 301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATACTCT 360
|||||||| |||||||||||| |||||||||||||| |||| |||| | |
Db 322 ATCAGCAGCCTGCAGGCGGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 381

Qy 361 --- TACACCTTCGGCCAAGGGACCAAGCTGGAAATAAAA 396
||| ||||| |||||||||||| || |||
Db 382 CCTCGGCTGCACCTTCGGCCAAGGGACCAAGGTGGAGATCAAA 423

RESULT 8
US-10-146-405-5
; Sequence 5, Application US/10146405
; Patent No. US20020173035A1
; GENERAL INFORMATION:
; APPLICANT: [illegible]
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; TITLE OF INVENTION: S SURFACE ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: CVI7440
; CURRENT APPLICATION NUMBER: US/10/146,405
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 5
; LENGTH: 390
; TYPE: DNA

; ORGANISM: Escherichia coli
US-10-146-305-5

Query Match 62.2%; Score 245.4; DB 9; Length 993;
Best Local Similarity 83.9%; Pred. No. 1.4e-74;
Matches 289; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 61 GAGATCTTGTTCATCATCATCCAGATCCTCTGCTGTGAAGCTTAATGACAGAGGGCCTGAT 120
Db 1 GAGATCTTGATGATCATCATCGATCCTCTGCTGTGAAGCTTAATGACAGAGGGCCTGAT 60

Qy 121 ATTATCTGCAAACTAATCATCATCTTCTGACACAAA 155
Db 61 ATTGACTGCAAACTGACCATCATCATCTTCTGACACAAA 95

Qy 181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
Db 121 TGGTACCAGCAGAAACCAGGGCAGCCTCCTGAACTGCTGATTTACTGGGCATCCACTAAG 180

Qy 241 GAATCTGGGGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
Db 181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy 301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCACGGCAATCTTATAATCTT 360
Db 241 ATCAGCAGTCTGCAAGCTGAAGACGTGGCAGTTTATTACTGCCAGGGCAATCTTATAATCTT 300

Qy 361 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
Db 301 CGCACGTTCGGACAGGGGACCAAGCTGGAAATAAAA 336

RESULT 9
US-10-056-052-17
; Sequence 17, Application US/10056052
; Publication No. US20030099956A1
; GENERAL INFORMATION:
; APPLICANT: PATIL, Joseph M
; APPLICANT: WITCHENS, Jeff I
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: PQ7006US04/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-056-052-17

Query Match 61.8%; Score 244.8; DB 9; Length 336;
Best Local Similarity 83.0%; Pred. No. 4.7e-74;
Matches 279; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 61 GAGATCTTGTTCATCATCATCCAGATCCTCTGCTGTGAAGCTTAATGACAGAGGGCCTGAT 120
Db 1 GAGATCTTGATGATCATCATCGATCCTCTGCTGTGAAGCTTAATGACAGAGGGCCTGAT 60

Qy 121 ATTATCTGCAAACTAATCATCATCTTCTGACACAAAGTTTACAGTTAAGGAGATCAAACGA 180
Db 61 ATTGACTGCAAACTGACCATCATCATCTTCTGACACAAAGTTTACAGTTAAGGAGATCAAACGA 120

Qy 181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
Db 121 TGGTACCAGCAGAAACCAGGGCAGCCTCCTGAACTGCTGATTTACTGGGCATCCACTAAG 180

Qy 241 GAATCTGGGGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
Db 181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy 301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCACGGCAATCTTATAATCTT 360
Db 241 ATCAGCAGTCTGCAAGCTGAAGACGTGGCAGTTTATTACTGCCAGGGCAATCTTATAATCTT 300

Qy 361 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
Db 301 CGCACGTTCGGACAGGGGACCAAGCTGGAAATAAAA 336

RESULT 10
US-09-995-529-1
; Sequence 1, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffry D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Yimu
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PatentSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(339)
US-09-995-529-1

Query Match 61.4%; Score 243; DB 9; Length 339;
Best Local Similarity 84.4%; Pred. No. 2e-73;
Matches 286; Conservative 0; Mismatches 50; Indels 3; Gaps 1;

Qy 61 GAGATCTTGTTCATCATCATCCAGATCCTCTGCTGTGAAGCTTAATGACAGAGGGCCTGAT 120
Db 1 GAGATCTTGATGATCATCATCGATCCTCTGCTGTGAAGCTTAATGACAGAGGGCCTGAT 60

Qy 121 ATTATCTGCAAACTAATCATCATCTTCTGACACAAAGTTTACAGTTAAGGAGATCAAACGA 180
Db 61 ATTGACTGCAAACTGACCATCATCATCTTCTGACACAAAGTTTACAGTTAAGGAGATCAAACGA 120

Qy 181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
Db 121 TGGTACCAGCAGAAACCAGGGCAGCCTCCTGAACTGCTGATTTACTGGGCATCCACTAAG 180

Qy 241 GAATCTGGGGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
Db 181 GAAT [illegible] 240

Qy 301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCACGGCAATCTTATAATCTT 360
Db 241 ATCAGCAGTCTGCAAGCTGAAGACGTGGCAGTTTATTACTGCCAGGGCAATCTTATAATCTT 300

Qy 361 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
Db 301 CGCACGTTCGGACAGGGGACCAAGCTGGAAATAAAA 336

RESULT 11
US-10-056-052-9

; Sequence 34, Application US/10060052
; Publication No. US2003009056A1
; GENERAL INFORMATION:
; APPLICANT: PATEL, Joseph M
; APPLICANT: BUTCHKO, Jeff F
; APPLICANT: ROMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLEA PROTEIN . . .
; FILE REFERENCE: P67-US041/BAS
; CURRENT APPLICATION NUMBER: US/10/060,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/284,826
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/285,115
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/284,113
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US 10/060,052

Query Match 54.9%; Score 237.4; DB 9; Length 336;
Best Local Similarity 81.8%; Pred. No. 1.3e-71;
Matches 271; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

Qy 62 ACATCGTGCTGACACAGTCTCCAGATCCCTGGCTGTAAGCCTAGGAGAGAGGGCCACTA 121
||||| |||||||||| ||| |||||||| |||||| | |||||
Db 1 ACATCAAAATCATCAGTCTCCATCATCCTGTCTGCATCTGTAGGAGACAGAGTCACCA 60

Qy 122 TTAGCTGCAAAGCCAGTCAGAGTGTGTCAACAGTAGAACCCTAGCAGCAACTACTTGGCCTT 181
| |||||| | |||||||| ||| | | | |||| || | |||||||||||| |
Db 61 TCAGTCTAAGTCCAGCAGTAAAGTGTTTATACAGCTCAATAAGAACTACTTGGCCTT 120

Qy 182 CGTACCAGCAGAAACCAGGGCAGCCTCCTAAAGTGCTGATCTACTGGGCATCCACTAGGG 241
|||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db 121 CGTACCAGCAGAAACCAGGGCAGCCTCCTAAAGTGCTGATCTACTGGGCATCCACTAGGG 180

Qy 242 AATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCA 301
|||||| |||||||||||| |||||||||||||||||||||||||||||||||||||||
Db 181 AATCTAGTGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCA 240

Qy 302 TCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATCTTATAATACTCCT 361
||| |||| | |||||||| |||||||||||||||||||||||||||||||||||| |||
Db 241 TCAGCAGTCTGCAACCTGAAGATGTTGCAACTTATTACTGTCAGCAATCTTATAATACTCCT 300

Qy 362 ACATTCGGCCAAGGGACCAAGGTGGAAATAAAA 396
|||||||||| |||||||||| ||||||||||||
Db 301 ACATTCGGCCAAGGGACCAAGCTGGAAATAAAA 335

RESULT 12
US/09/897,511A/34
; Sequence 34, Application US/09897511A
; Publication No. US2002009708A1
; GENERAL INFORMATION:
; APPLICANT: Brewer, Robert
; APPLICANT: Mercer, Linda
; APPLICANT: Block, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Expression Vectors
; FILE REFERENCE: CALA 04415
; CURRENT APPLICATION NUMBER: US/09/897,511A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,851
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 34
; LENGTH: 9511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US 09/897-511A 34

Query Match 59.5%; Score 235.6; DB 9; Length 9511;
Best Local Similarity 82.1%; Pred. No. 2.3e-70;
Matches 271; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

Qy 57 GACATCGTGCTGACACAGTCTCCAGATCCCTGGCTGTAAGCCTAGGAGAGAGGGCCACTATA 120
| ||| || |||||||||| |||||||||| | || |||||||||| || | |
Db 5704 GAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC 5763

Qy 121 TTAGCTGCAAAGCCAGTCAGAGTGTGTCAACAGTAGAACCCTAGCAGCAACTACTTGGCCTT 180
||||| ||||| |||||| | | |||| | || |||||||| || |||||||||
Db 5764 TGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACAATAAGAACTATTTAGCTTGGTAT 5823

Qy 181 CGTACCAGCAGAAACCAGGGCAGCCTCCTAAAGTGCTGATCTACTGGGCATCCACTAGGGAAT 240
||||||||||||||| |||||||||| |||| || |||||||||| || |||||||
Db 5824 CAGCAGAAACCAGGACAGCCTCCTAAGCTGCTGATTTACTGGGCATCTACTAGGGAATCC 5883

Qy 241 GGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAG 300
|||||||||| |||||||||| || |||||||||||||||||||||||||||||||||||
Db 5884 CGGGTCCCTGATCGAATCAGTGGCAGCGGTCTGGGACAGATTCACTCTCACCATCAGCAG 5943

Qy 301 TCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCAGCAATCTTATAATACTCCTACATTC 360
|| |||||||||||||| |||||||||||||||| |||| ||||| | | | |||
Db 5944 TCTGCAACCTGAAGATGTTGCAACTTATTACTGTCAGCAATCATATAGTACTCCGTGGACG 6003

Qy 361 GGCCAAGGGACCAAGGTGGAAATAAAA 396
||||| || |||||||||||||||| |||
Db 6004 GGCCAGGGCACCAAGCTGGAAATCAAA 6031

RESULT 13
US/09/897,006/34
; Sequence 34, Application US/09897006
; Patent No. US20020106729A1
; GENERAL INFORMATION:
; APPLICANT: Block, Gregory
; TITLE OF INVENTION: Expression Vectors
; FILE REFERENCE: CALA 06415
; CURRENT APPLICATION NUMBER: US/09/897,006
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,851
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 9511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US 09/897,006/34

Query Match 59.5%; Score 235.6; DB 10; Length 9511;
Best Local Similarity 82.1%; Pred. No. 2.3e-70;
Matches 271; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

Qy 57 GACATCGTGCTGACACAGTCTCCAGATCCCTGGCTGTAAGCCTAGGAGAGAGGGCCACTATA 120
| ||| || |||||||||| |||||||||| | || |||||||||| || | |
Db 5704 GAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC 5763

Qy 121 TTAGCTGCAAAGCCAGTCAGAGTGTGTCAACAGTAGAACCCTAGCAGCAACTACTTGGCCTT 180
||||| ||||| |||||| | | |||| | || |||||||| || |||||||||
Db 5764 TGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACAATAAGAACTATTTAGCTTGGTAT 5823

Qy 181 CGTACCAGCAGAAACCAGGGCAGCCTCCTAAAGTGCTGATCTACTGGGCATCCACTAGGGAAT 240
||||||||||||||| |||||||||| |||| || |||||||||| || |||||||
Db 5824 CAGCAGAAACCAGGACAGCCTCCTAAGCTGCTGATTTACTGGGCATCTACTAGGGAATCC 5883

Qy 241 GGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAG 300
|||||||||| |||||||||| || |||||||||||||||||||||||||||||||||||
Db 5884 CGGGTCCCTGATCGAATCAGTGGCAGCGGTCTGGGACAGATTCACTCTCACCATCAGCAG 5943

Qy 301 TCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCCAGCAATCTTATAATACTCCTACATTC 360
|| |||||||||||||| |||||||||||||||| |||| ||||| | | | |||
Db 5944 TCTGCAACCTGAAGATGTTGCAACTTATTACTGTCAGCAATCATATAGTACTCCGTGGACG 6003

Qy 361 GGCCAAGGGACCAAGGTGGAAATAAAA 396
||||| || |||||||||||||||| |||
Db 6004 GGCCAGGGCACCAAGCTGGAAATCAAA 6031

RESULT 14
; SEQUENCE: 8
; Sequence 8, Application US/09/998,831
; Patent No. US20020119154A1
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
; TITLE OF INVENTION: INHIBITING VEGF
; FILE REFERENCE: 4001.002584
; CURRENT APPLICATION NUMBER: US/09/998,831
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/561,108
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNthetic
; OTHER INFORMATION: OLIGONUCLEOTIDE

Query Match 59.8%; Score 285; DB 10; Length 517;
Best Local Similarity 82.3%; Pred. No. 1.1e-76;
Matches 261; Conservative 0; Mismatches 56; Indels 0; Gaps 1;

RESULT 15
US-10-056-052-13
; Sequence 13, Application US/10056052
; Publication No. US20030099651A1

; GENERAL INFORMATION:
; APPLICANT: PATEL, Joseph M
; APPLICANT: BEECHEN, Joel I
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE TEA PROTEIN . . .
; FILE REFERENCE: P03869US01/BAS
; CURRENT APPLICATION NUMBER: US/10/056,052
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-056-052-13

Query Match 59.1%; Score 284.2; DB 9; Length 336;
Best Local Similarity 81.2%; Pred. No. 2.1e-70;
Matches 272; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Search completed: June 18, 2003, 00:41:14
Job time : 161.02 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 13:38:03 ; Search time 3.216 Seconds
(without alignments)
3612.472 Million cell updates/sec

Title: US-09-249-011B-7
Perfect score: 396
Sequence: 1 atggattcacaaggcccaggt.....cgtacccaaaaaaaaaaaaa 396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441962 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 88224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/iss_na/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/iss_na/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/iss_na/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/iss_na/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/iss_na/7_COMB.seq:*
6: /cgn2_6/ptodata/1/iss_na/8911lost.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	396	100.0	940	1	US-08-353-400-24	Sequence 24, Appl
2	281.2	71.0	442	3	US-08-929-856-65	Sequence 65, Appl
3	279.8	70.7	1443	2	US-08-403-853-19	Sequence 19, Appl
4	279	70.5	427	4	US-09-301-593-23	Sequence 23, Appl
5	279	70.5	465	3	US-08-951-068-35	Sequence 35, Appl
6	279	70.5	8068	4	US-09-301-593-27	Sequence 27, Appl
7	277.4	70.1	499	5	PCT-US93-11611-1	Sequence 1, Appli
8	275.8	69.6	870	2	US-08-403-853-15	Sequence 15, Appl
9	270.8	68.4	330	4	US-08-967-001B-4	Sequence 4, Appli
10	270.8	68.4	330	4	US-09-496-301-4	Sequence 4, Appli
11	270.6	68.3	864	4	US-09-423-439-47	Sequence 47, Appl
12	270.6	68.3	2019	4	US-09-423-439-31	Sequence 31, Appl
13	270.6	68.4	2025	4	US-09-423-439-47	Sequence 47, Appl
14	267.2	67.5	842	3	US-08-929-856-188	Sequence 188, App
15	267.2	67.5	1701	2	US-07-916-098A-54	Sequence 54, Appl
16	267.2	67.5	1701	2	US-07-916-098A-55	Sequence 55, Appl
17	264.6	66.8	427	2	US-08-308-494A-24	Sequence 24, Appl
18	264.6	66.8	499	4	US-08-579-378A-1	Sequence 1, Appli
19	264.6	66.8	499	5	PCT-US93-11612-1	Sequence 1, Appli
20	252.2	63.7	342	3	US-08-951-068-25	Sequence 25, Appl
21	250.2	63.2	402	4	US-09-587-626-8	Sequence 8, Appli
22	248.6	62.8	8068	4	US-09-301-593-35	Sequence 35, Appl
23	248.2	62.7	444	2	US-07-916-098A-84	Sequence 84, Appl
24	247	62.4	5703	1	US-08-470-420A-55	Sequence 55, Appl
25	247	62.4	5703	1	US-08-470-110A-50	Sequence 50, Appl
26	247	62.4	5703	1	US-08-667-769A-50	Sequence 50, Appl
27	247	62.4	5703	2	US-08-940-871-50	Sequence 50, Appl
28	247	62.4	5703	3	US-08-637-642-50	Sequence 50, Appl
29	247	62.4	5703	5	PCT-US95-17082A-50	Sequence 50, Appl
30	244.6	61.8	336	2	US-07-916-098A-14	Sequence 14, Appl
31	244.4	61.8	339	3	US-08-485-749A-15	Sequence 15, Appl
32	241	60.9	340	2	US-07-916-098A-13	Sequence 13, Appl
33	238.6	60.3	795	2	US-08-822-028-11	Sequence 11, Appl
34	238.6	60.3	795	4	US-08-479-285-11	Sequence 11, Appl
35	238.2	60.2	342	2	US-08-428-267A-25	Sequence 25, Appl
36	238.2	60.2	342	4	US-07-987-264-15	Sequence 15, Appl
37	235	59.3	347	4	US-09-561-500-8	Sequence 8, Appli
38	235	59.3	347	4	US-09-561-108-8	Sequence 8, Appli
39	235	59.3	347	4	US-09-561-526-8	Sequence 8, Appli
40	233.4	58.9	339	5	PCT-US93-08435-3	Sequence 3, Appli
41	232.8	58.8	924	2	US-08-860-174A-9	Sequence 9, Appli
42	232.8	58.8	924	4	US-09-171-025-26	Sequence 26, Appl
43	232.8	58.8	930	1	US-09-171-025-3	Sequence 3, Appli
44	232.6	58.7	1706	2	US-08-860-174A-11	Sequence 11, Appl
45	232.6	58.7	1706	4	US-09-171-025-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-353-400-24
; Sequence 24, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 940 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-353-400-24

Query Match 83.8%; Score 332; DB 1; Length 940;
Best Local Similarity 89.9%; Pred. No. 2.9e-97;
Matches 456; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 1 ATGGATTCACAAGGCCCAGGTTCCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGG 60
Db 1 ATGGATTCACAAGGCCCAGGTTCCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGG 60

Qy 61 GACATTGGGCTGACACAGTCTCCAGATCCCTGGCTGTAACCTTAGGAGAGAGGGCCACT 120
Db 61 GACATTGGGCTGACACAGTCTCCAGATCCCTGGCTGTAACCTTAGGAGAGAGGGCCACT 120

Qy 121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAAACCCGAGAGAACTACTTGGCT 180
Db 121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAAACCCGAGAGAACTACTTGGCT 180

Qy 181 TGGTACCAACAGAAACCAGGGCAGCCTCCTAAACTGCTGATACTACTCGGGATCCACTAGG 240
Db 181 TGGTACCAACAGAAACCAGGGCAGCCTCCTAAACTGCTGATACTACTCGGGATCCACTAGG 240

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Db          190 TGGTACTACTAGAGACTAGGGCAGTCTCCTAAACTGCTGATCTATTGGGCATCCACTAGG 249

Qy          241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          250 ACATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 309

Qy          301 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          310 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTC 369

Qy          361 TACACGTTCGGACAGGGGACCAAGCTGGAGATCAAAA 397
                |||||||||||||||||||||||||||||||||||||
Db          370 TACACGTTCGGACAGGGGACCAAGCTGGAGATCAAAA 406

RESULT 2
US-08-929-856-65
; Sequence 65, Application US/08929856
; Patent No. 5840568
;  GENERAL INFORMATION:
;    APPLICANT:  Bhatt, Andrew
;    APPLICANT:  Rose, Floyd
;    TITLE OF INVENTION:  DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
;    TITLE OF INVENTION:  ROLLING TEMPLATES
;    NUMBER OF SEQUENCES:  100
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LERNER, DAVID, LITTENBERG, KRUMHOLZ &
;      ADDRESSEE:  MENTLIK
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07090
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/929,856
;      FILING DATE:  15-SEP-1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bailey, Diana D.
;      REGISTRATION NUMBER:  33,881
;      REFERENCE/DOCKET NUMBER:  [illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-654-5000
;      TELEFAX:  908-654-7866
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  N
;      LOCATION:  1..41
US-08-929-856-65

  Query Match             71.5%;  Score 284.2;  DB 3;  Length 442;
  Best Local Similarity   90.2%;  Pred. No. 9.3e-82;
  Matches  303;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          61 GACATCTGCTCGACTACAGTCTCCAGATCTCCCTCCTCAAGCTTACGTACATACGACGCC 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GACATCTGCATGACTACAGTCTCCATCTCCCTCCTCGCTGTCAGCACGAGACGAAGGCCACT 60

Qy         121 ATTAACATCAAAATTACTCATCAGAGTCTCCTCAACACTAACGTTGCTGTTTATCACTGCGTT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ATGAGCTCCAAAATCACTCAGATCTCGTCCAACACTAACGCCGAAACAACTTCTTGGCCT 120

Qy         181 GGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGTACAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTC 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTC 300

Qy         361 TACACGTTCGGACAGGGGACCAAGCTGGAGATCAAAA 397
               |||||||||||||||||||||||||||||||||||||
Db         301 TACACGTTCGGACAGGGGACCAAGCTGGAGATCAAAA 337

RESULT 3
US-08-403-853-19
; Sequence 19, Application US/08403853
; Patent No. 5844094
;  GENERAL INFORMATION:
;    APPLICANT:  HUDSON, Peter J.
;    APPLICANT:  LAH, Maria
;    APPLICANT:  KORRT, Alex A.
;    APPLICANT:  IRVING, Robert A.
;    APPLICANT:  ATWELL, John L.
;    APPLICANT:  MALBY, Robyn L.
;    APPLICANT:  POWER, Barbara E.
;    APPLICANT:  COLMAN, Peter M.
;    TITLE OF INVENTION:  TARGET BINDING POLYPEPTIDE
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,853
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/AU93/00491
;      FILING DATE:  24-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PL 1974
;      FILING DATE:  25-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  [illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1443 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-403-853-19

  Query Match             70.7%;  Score 279.8;  DB 2;  Length 1443;
  Best Local Similarity   84.6%;  Pred. No. 2e-80;
  Matches  314;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;
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Qy          29 TATTGCTCATGCTATGGTATCTGGCACCTGTGGGGACATTGTGCTGACACAGTCTCCAG 88
               |||| | ||| |  | |  |||   | ||||| |   || ||||||||||||
Db         534 TATTACTGTTACTCTTATGGTGGTAACAAAGCCGACATTGTCATGACACAGTCTCCAT 593

Qy          89 ATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACTATTAGCTGCAAATCCAGCCAGAGTC 148
               ||||||||||||     |||||||| || |||||| ||||||| ||||||||||||||
Db         594 CCTCCCTGGCTGTGTCACTAGGAGACAAGGTCACTATGAGCTGCAGATCCAGTCAGAGTC 653

Qy         149 TGTCAACACAGTAGAACCCGAGAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGC 208
               || ||||||||||||||| ||||||||||| ||||||||||||||||||||||||||||
Db         654 TGTTCAACAGTAGAACCCGAAAGAACTACTTGACTTGGTACCAGCAGAAACCAGGGCAGT 713

Qy         209 CCTCCTAAACTGGTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCA 268
               |||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         714 CCTCCTAAACCGGTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCA 773

Qy         269 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGGCTGAAGACG 328
               |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         774 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGATG 833

Qy         329 TGGCAGTTTATTACTGCACGCAATCTTATAATCCTTTCACGTTCGGACAGGGACCAAGG 388
               ||||| ||||||||||| ||||||||||||||   |||||||    || |||||||
Db         834 TGGCAGATTATTACTGCAAGCAATATTATAATCCTTTCACGTTCGGAGGGACCAAGG 893

Qy         389 TGGAAATAAAA 399
               |||| |||||
Db         894 TGGAAATTAAA 904


RESULT 4
US-09-401-543-23
; Sequence 23, Application US/09351594A
; Patent No. 6156677
; GENERAL INFORMATION:
;  APPLICANT: Park, John E.
;  APPLICANT: Garin-Chesa, Pilar
;  APPLICANT: Bamberger, Uwe
;  APPLICANT: Leger, Olivier
;  APPLICANT: Saldanha, Jose W.
;  APPLICANT: Rettig, Wolfgang J.
;  TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
;  FILE REFERENCE: 065_199903US1
;  CURRENT APPLICATION NUMBER: US/09/351,594A
;  CURRENT FILING DATE: 1999-04-29
;  EARLIER APPLICATION NUMBER: PCT/EP97/[illegible]
;  EARLIER FILING DATE: 1998-04-30
;  EARLIER APPLICATION NUMBER: US 60/046,049
;  EARLIER FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 427
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-401-543-23

  Query Match             70.5%;  Score 279;  DB 4;  Length 427;
  Best Local Similarity   83.0%;  Pred. No. 2.3e-80;
  Matches  331;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    1;

Qy           1 ATTGATTCACAGGCCCAGGTCTTATATTGCTGCTCTATGGTTATCTGGCACCTGTGGGG 60
               ||.|||||||||||||||||||| ||  || |||| |||||||||||||| |||||||||
Db          16 ATGGATTCACAGGCCCAGGTCTTTATCTTACTGCTCTATGGGTTATCTGGTACCTGTGGGG 75

Qy          61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACT 120
               |||||||| || |.|||||||||   |||| ||||      | |||||| || |||
Db          76 GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGCTGGAGAGAAGGTTACT 135

Qy         121 ATTAGCTGCAAATCCAGCCAGAGTCTGTCAACACAGTAGAACCCGAGAGAACTACTTGGCT 180
               || |||||||| |||||||||| || |  | ||| | |  | ||||||||||||
Db         136 ATGAGCTGCAAGTCCAGCCAGAGCCTTTTATATAGCTCGTAATCAAAAGAACTACTTGGCC 195

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
               |||| |||||||| |||||||  ||||||||||||||| | |||||||||||||||||
Db         196 TGGCTCCAGCAGAAGCCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCATCCACTAGG 255

Qy         241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               |||||||||||||||||||||||| |  ||||||||| |||||| ||||||| |||||
Db         256 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATTTGGGACGGATTTCAATCTCACC 315

Qy         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAATCTTATA   AT 357
               .|.|||||| |||||||||| ||| |||||||||| ||||   |.|| || ||   ||
Db         316 ATCAGCAGTGTGCAGGCTGAAGACGTGGCAGTTTATGACTGTCAGCAAGATTATGAC TAT 375

Qy         358 CCTTTCACGTTCGGACAGGGACCAAGGTGGAAATAAAA 396
               |   |||||||||    |||||||| |||| | |||
Db         376 CCGCTCACGTTCGGTGGTGGCACCAAGCTGGAAATCAAA 414


RESULT 5
US-08-513-968-35
; Sequence 35, Application Us/08513968
; Patent No. 6111143
;  GENERAL INFORMATION:
;    APPLICANT:  EDA, Yasuyuki
;    APPLICANT:  MUKAI, Hiroaki
;    APPLICANT:  MAKISUMI, Keiichi
;    APPLICANT:  SHIOSAKI, Kouichi
;    APPLICANT:  OSAIOMI, Kiyoshi
;    APPLICANT:  KIMACHI, Kazuhiko
;    APPLICANT:  HIGUCHI, Hirofumi
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  ANTI-HIV MONOCLONAL ANTIBODY
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,968
;      FILING DATE:  11-SEP-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 78916/1993
;      FILING DATE:  11-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROWDY, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  EDA 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  463 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..463
US-08-513-968-35

  Query Match             70.5%;  Score 279;  DB 3;  Length 463;
  Best Local Similarity   83.0%;  Pred. No. 2.5e-80;
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  Matches  331;  Conservative    0;  Mismatches   56;  Indels    5;  Gaps    1;

Qy          1 ATGGATTCACAGGTCCAGGTTCTTATATTGCTTGTTGCTATGGGTATCTGGACCTGTGGG 60
              |||||| |||||||   | ||| || || |  ||||| | |||||||||||| ||||||||
Db         13 ATGTAATGCACAGATTCTGGTTGTCATGTGTCTGTTCTGGGTATTGGTACCTGTGGG 72

Qy         61 GACATGTGCTGGACAACATGTCTACAATCTCCTGGCTGAAGCTTACAGAAAGGGGCCACT 120
              |||||||| ||||||||||||    |||||| ||| |    |||||| || ||||||||||
Db         73 GACATTGTGATGACAACAGTCTCATCTCCTGGACTGTGACAGCAGGAGAAGCTCACT 132

Qy        121 ATTAGCTGCAAAATCAGTCAGAGTCTGCTAACACTAACAACCCGAGAGAACTACTTGGCT 180
              || |||||||| ||||||||||||| | ||||| ||    | | ||||||||||| |
Db        133 ATGAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAGATCAAAAGAACTACTTGACC 192

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              |||||||||||||||||||||||||||||| |||||| |||||||||||| ||
Db        193 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGTTGATCTATGGGGCATCCACTGGG 252

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGAACAGATTTCACTCTCACC 300
              |||||||| ||||||||||||||  |||||||||||||  ||||||||||||||||||||
Db        253 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGAAACAGATTTCACTCTCACC 312

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAAATCTTATA---AT 357
              |||||||| |||||||||||||| ||||||||||||||  | |   ||||   ||
Db        313 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGAATGATTATAGTTAT 372

Qy        358 CTTTACACGTTCGGACAGGGGACCAAGCTGGAAATAAAA 396
              |  |  ||||||||    || ||||  |||||| |||
Db        373 CCGCTGACGTTCGGTGGAGGCACCAAGGTGGAGATCAAA 411


RESULT 6
US-09-249-011B-7
; Sequence 7, Application US/09249011B
; Patent No. 6420377
; GENERAL INFORMATION:
;  APPLICANT: Park, Edmund E.
;  APPLICANT: Green Thesis, Peter
;  APPLICANT: Bamberger, Uwe
;  APPLICANT: Leeper, Clifford
;  APPLICANT: Subbanna, Jose W.
;  APPLICANT: Reddig, Wolfgang J.
;  TITLE OF INVENTION: FAP Specific Antibody with Improved Producibility
;  FILE REFERENCE: 06521.1890001
;  CURRENT APPLICATION NUMBER: US/09/249,011B
;  CURRENT FILING DATE: 1999-04-29
;  EARLIER APPLICATION NUMBER: EP 98107920.4
;  EARLIER FILING DATE: 1998-04-30
;  EARLIER APPLICATION NUMBER: US 60/080,449
;  EARLIER FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
;  LENGTH: 8068
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-249-011B-7

  Query Match             79.5%;  Score 277;  DB 4;  Length 8068;
  Best Local Similarity   83.6%;  Pred. No. 7.2e-80;
  Matches  331;  Conservative    0;  Mismatches   56;  Indels    5;  Gaps    1;

Qy          1 ATGGATTCACAGGTCCAGGTTCTTATATTGCTTGTTGCTATGGGTATCTGGACCTGTGGG 60
              |||||| |||||||   | ||| || || |  ||||| | |||||||||||| ||||||||
Db       1709 ATGTAATGCACAGATTCTGGTTGTCATGTGTCTGTTCTGGGTATTGGTACCTGTGGG 1768

Qy         61 GACATTGTGCTGACAACAGTCTCATCTCCTGGCTGAAGCTTACAGAAAGGGGCCACT 120
              |||||||| || |||||||||    |||| ||||     | |||||| || |||
Db       1769 GACATTGTGATGACACAGTCTCCAGCCTCCCTGGCTGTGTCTCTAGGGCAGAGGGCCACC 1828

Qy        121 ATTAGCTGCAAAATCAGTCAGAGTCTGCTAACACTAACAACCCGAGAGAACTACTTGGCT 180
              || |||||||| ||||||||||||| | ||||| ||    | | ||||||||||| |
Db       1829 ATCAACTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAGATCAAAAGAACTACTTGACC 1888

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              |||||||||||||||||||||||||||||| |||||| |||||||||||| ||
Db       1889 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGTTGATCTATGGGGCATCCACTGGG 1948

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGAACAGATTTCACTCTCACC 300
              |||||||| ||||||||||||||  |||||||||||||  ||||||||||||||||||||
Db       1949 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGAAACAGATTTCACTCTCACC 2008

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAAATCTTATA---AT 357
              |||||||| |||||||||||||| ||||||||||||||  | |   ||||   ||
Db       2009 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGAATGATTATAGTTAT 2068

Qy        358 CTTTACACGTTCGGACAGGGGACCAAGCTGGAAATAAAA 396
              |  |  ||||||||    || ||||  |||||| |||
Db       2069 CCGCTGACGTTCGGTGGAGGCACCAAGGTGGAGATCAAA 2107


RESULT 7
PCT-US93-11611-1
; Sequence 1, Application PC/TUS9311611
;  GENERAL INFORMATION:
;    APPLICANT:  Co, Man Sung
;    APPLICANT:  Landolfi, Nicholas F.
;    TITLE OF INVENTION:  Humanized Antibodies Reactive with CD18
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patentin Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/11611
;      FILING DATE:  30-NOV-1993
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/983,949
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-45
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  399 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..399
PCT-US93-11611-1

  Query Match             79.1%;  Score 275.4;  DB 5;  Length 399;
  Best Local Similarity   82.7%;  Pred. No. 7.2e-80;
  Matches  330;  Conservative    0;  Mismatches   69;  Indels    5;  Gaps    1;

Qy          1 ATGGATTCACAGGTCCAGGTTCTTATATTGCTTGTTGCTATGGGTATCTGGACCTGTGGG 60
              |||||||||||||||||||||||||||||| || ||||||||||||| ||||| |||
Db          1 ATGGATTCACAGGTCCAGGTTCTTATATTGCTTGTTGCTATGGGTATCTGGACAGTGGG 60

Qy         61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCCTTGGCGAGAGGGCCACT 120
              |||||||| || |||||||||    |||| ||||     | |||||| || |||
Db         61 GACATTGTGATGACACAGTCTCCAGCCTCCCTGGCTGTGTCTCTAGGGCAGAGGGCCACC 120

Qy        121 ATTAGCTGCAAAATCAGTCAGAGTCTGCTAACACTAACAACCCGAGAGAACTACTTGGCT 180
              || |||||||| ||||||||||||| | ||||| ||    | | ||||||||||| |
Db        121 ATCAACTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAGATCAAAAGAACTACTTGACC 180

Qy        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240
              |||||||||||||||||||||||||||||| |||||| |||||||||||| ||
Db        181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGTTGATCTATGGGGCATCCACTGGG 240

Qy        241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGAACAGATTTCACTCTCACC 300
              |||||||| ||||||||||||||  |||||||||||||  ||||||||||||||||||||
Db        241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGAAACAGATTTCACTCTCACC 300

Qy        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAAATCTTATA---AT 357
              |||||||| |||||||||||||| ||||||||||||||  | |   ||||   ||
Db        301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGAATGATTATAGTTAT 360

Qy        358 CTTTACACGTTCGGACAGGGGACCAAGCTGGAAATAAAA 396
              |  |  ||||||||    || ||||  |||||| |||
Db        361 CCGCTGACGTTCGGTGGAGGCACCAAGGTGGAGATCAAA 399
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Db        61 GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTTACT 120

Qy       121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180

Db       121 ATGAGCTGCAAGTCCAGTCAGAGCCTTTTACTAGCTGTGTCAGTTGGAGAGAAGGTTACT 180

Qy       181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240

Db       181 TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCATCTACTAGG 240

Qy       241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300

Db       241 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300

Qy       301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAATCTTATA---AT 357

Db       301 ATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAATATTATAGCTAT 360

Qy       358 CTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396

Db       361 --ATTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAA 399
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RESULT 8
US-08-403-853-15
; Sequence 15, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORTT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 36786/180/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 870 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 40..834
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..834
US-08-403-853-15

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  Query Match             69.6%;  Score 275.8;  DB 2;  Length 870;
  Best Local Similarity   89.0%;  Pred. No. 3.2e-79;
  Matches  298;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy        61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGTTAGGAGAGAGGGCCACT 120

Db       463 GACATCGTCATGTCACAGTCTCCATCCTCCCTGGCTGTGTCAGTAGGAGAGAAGGTCACT 522

Qy       121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180

Db       523 ATGAGCTGCAGATCCAGTCAGAGTCTGTTCAACAGTAGAACCCGAAAGAACTACTTGACT 582

Qy       181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 240

Db       583 TGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACCGCTGATCTACTGGGCATCCACTAGG 642

Qy       241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300

Db       643 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 702

Qy       301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCACGCAATCTTATAATCTT 360

Db       703 ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGATTATTACTGCAAGCAATCTTATAATCTT 762

Qy       361 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAA 395

Db       763 CGGACGTTCGGTGGAGGCACCAAGCTGGAAATTAA 797
```

RESULT 9
US-08-957-001B-4
; Sequence 4, Application US/08957001B
; Patent No. 6228621
; GENERAL INFORMATION:
; APPLICANT: Williams, William V.
; APPLICANT: Madaio, Michael
; APPLICANT: Weiner, David B.
; TITLE OF INVENTION: IMPROVED VACCINES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621.s
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,001B
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,592
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-3303

```
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215 568 3100
;       TELEFAX:  215 568 3439
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  330 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  both
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..330
US-09-496-301-3

  Query Match             68.4%;  Score 270.8;  DB 4;  Length 330;
  Best Local Similarity   88.8%;  Pred. No. 8.9e-78;
  Matches  293;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGATGGGCCACT 120
               ||||||||| | ||||||||||    |||||||||      |||||||| || ||||
Db           1 GACATTCTGATATCACAGTCTCCATCCACCCTGGCTGTGTCAGCAGGAGAGAAGGTCACT 60

Qy         121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACAAGCCGAGAGAACTACTTGGCT 180
               || | ||||||||||||||||||| ||||||||||||||| ||||||||||||||||||
Db          61 ATGAACTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACAAGCCGAAAGAACTACTTGGCT 120

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAAACTGCTGATCTACTGGGCATCCACTAGG 240
               |||| |||||||||||||||||| ||| |||||||||||||||||||||||||||||||
Db         121 TGGTTCCAGCAGAAACCAGGGCAGTCTCCTAAAGCTGCTGATCTACTGGGCATCCACTAGG 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGGCAATCTTATAATCTT 360
               ||||||||| |||||||||||||| |||||||||||||||| |||||||||| |||| ||
Db         241 ATCAGCAGCCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAACAATCTTATTATCTT 300

Qy         361 TACACGTTCGGACAGGGGACCAAGCTGGAA 390
               |||||||   || |||| | |||| |
Db         301 CCGACGTTCGGTGGAGGCACCAAGCTGGAA 330


RESULT 10
US-09-496-301-4
; Sequence 4, Application US/09496301
  Patent No. 6248575
  GENERAL INFORMATION:
    APPLICANT:  Wallace, William V.
    APPLICANT:  Mullins, Michael
    APPLICANT:  Weiner, David B.
    TITLE OF INVENTION:  IMPROVED VACCINES
    NUMBER OF SEQUENCES:  27
    CORRESPONDENCE ADDRESS:
      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & Nor
      STREET:  One Liberty Place, 46th Floor
      CITY:  Philadelphia
      STATE:  Pennsylvania
      COUNTRY:  USA
      ZIP:  19103
    COMPUTER READABLE FORM:
      MEDIUM TYPE:  Floppy disk
      COMPUTER:  IBM PC compatible
      OPERATING SYSTEM:  Windows
      SOFTWARE:  Word perfect
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/09/496,301
      FILING DATE:
      CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  08/827,992
      FILING DATE:  23-OCT-1997
;       APPLICATION NUMBER:  US 60/029,592
;       FILING DATE:  23-OCT-1996
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DeLuca, Mark
;       REGISTRATION NUMBER:  33,229
;       REFERENCE/DOCKET NUMBER:  DEN 3333
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-568-3100
;       TELEFAX:  215-568-3439
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  330 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  both
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..330
US-09-496-301-4

  Query Match             68.4%;  Score 270.8;  DB 4;  Length 330;
  Best Local Similarity   88.8%;  Pred. No. 8.9e-78;
  Matches  293;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGATGGGCCACT 120
               ||||||||| | ||||||||||    |||||||||      |||||||| || ||||
Db           1 GACATTCTGATATCACAGTCTCCATCCACCCTGGCTGTGTCAGCAGGAGAGAAGGTCACT 60

Qy         121 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACAAGCCGAGAGAACTACTTGGCT 180
               || | ||||||||||||||||||| ||||||||||||||| ||||||||||||||||||
Db          61 ATGAACTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACAAGCCGAAAGAACTACTTGGCT 120

Qy         181 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAAACTGCTGATCTACTGGGCATCCACTAGG 240
               |||| |||||||||||||||||| ||| |||||||||||||||||||||||||||||||
Db         121 TGGTTCCAGCAGAAACCAGGGCAGTCTCCTAAAGCTGCTGATCTACTGGGCATCCACTAGG 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGGCAATCTTATAATCTT 360
               ||||||||| |||||||||||||| |||||||||||||||| |||||||||| |||| ||
Db         241 ATCAGCAGCCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAACAATCTTATTATCTT 300

Qy         361 TACACGTTCGGACAGGGGACCAAGCTGGAA 390
               |||||||   || |||| | |||| |
Db         301 CCGACGTTCGGTGGAGGCACCAAGCTGGAA 330


RESULT 11
US-09-423-439-47
; Sequence 47, Application US/09423439
; Patent No. 6339070
;   GENERAL INFORMATION:
;         APPLICANT: EMERY, Stephen Charles
;                    BLAKEY, David Charles
;         TITLE OF INVENTION: CHEMICAL COMPOUNDS
;         NUMBER OF SEQUENCES: 60
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Pillsbury Winthrop, L.L.P.
;              STREET: 1100 New York Ave., N.W.
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: U.S.A.
;              ZIP: 20005
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: MS Word
;         CURRENT APPLICATION DATA:
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;               APPLICATION NUMBER: US/09/423,439
;               FILING DATE: 04-Nov-1999
;               CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: PCT/GB98/01294
;               FILING DATE: 05-MAY-1998
;               APPLICATION NUMBER: GB 9709421.5
;               FILING DATE: 10-MAY-1997
;     INFORMATION FOR SEQ ID NO: 47:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 864 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;          MOLECULE TYPE: other nucleic acid
;          SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-423-439-47

  Query Match             68.8%;  Score 270.6;  DB 4;  Length 864;
  Best Local Similarity   86.0%;  Pred. No. 1.5e-77;
  Matches  309;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          48 TGGTACCTGTGGGGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGG 107
               |||| | |    |||||||  ||| ||||||||||    ||||||||||      |||
Db         462 TGGGAGGAATCTGACATTGAGCTCTCACAGTCTCATCTCCTCGGTGTCAGCAGG 521

Qy         108 AGAGAGGGCCACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGA 167
               |||| || ||| || ||||||||||||||||||||| ||| |||||||||||||| |
Db         522 AGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTCCTCAACAGTAGAACCCGAAA 581

Qy         168 GAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTG 227
               |||||||||||||||||||||||||| |||||||| ||||||||||||||||||| ||
Db         582 GAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTG 641

Qy         228 GGCATCGACTAGGGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGA 287
               |||||||||||||  |||||||||||||||||||||||  ||||||||||||||||||
Db         642 GGCATCCACTAGGACATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGA 701

Qy         288 TTTCACTCTCACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCA 347
               ||||| |||||||||||||||| |||||||||||| ||||| |||||||||||| |||
Db         702 TTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAATTTATTACTGTAAGCA 761

Qy         348 ATTTATAATACTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
               ||||||| ||||  |||||||   || |||| | || | | ||||
Db         762 ATTTATACTCTTCGGCACGTTCGGTGGAGGCACCAAGCTGGAGATCAAA 810


RESULT 12
US-09-423-439-41
; Sequence 41, Application US/09423439
; Patent No. 6390670
;   GENERAL INFORMATION:
;        APPLICANT: EMERY, Stephen Charles
;                   BLAKEY, David Charles
;        TITLE OF INVENTION: CHEMICAL COMPOUNDS
;        NUMBER OF SEQUENCES: 60
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Winthrop, L.L.P.
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/423,439
;             FILING DATE: 04-Nov-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB98/01294
;             FILING DATE: 05-MAY-1998
;             APPLICATION NUMBER: GB 9709421.5
;             FILING DATE: 10-MAY-1997
;     INFORMATION FOR SEQ ID NO: 41:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 2019 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;          MOLECULE TYPE: other nucleic acid
;          SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-423-439-41

  Query Match             68.8%;  Score 270.6;  DB 4;  Length 2019;
  Best Local Similarity   86.0%;  Pred. No. 2.2e-77;
  Matches  309;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          48 TGGTACCTGTGGGGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGG 107
               |||| | |    |||||||  ||| ||||||||||    ||||||||||      |||
Db         453 TGGGAGGAATCTGACATTGAGCTCTCACAGTCTCATCTCCTCGGTGTCAGCAGG 512

Qy         108 AGAGAGGGCCACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGA 167
               |||| || ||| || ||||||||||||||||||||| ||| |||||||||||||| |
Db         513 AGAGAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTCCTCAACAGTAGAACCCGAAA 572

Qy         168 GAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTG 227
               |||||||||||||||||||||||||| |||||||| ||||||||||||||||||| ||
Db         573 GAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTG 632

Qy         228 GGCATCGACTAGGGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGA 287
               |||||||||||||  |||||||||||||||||||||||  ||||||||||||||||||
Db         633 GGCATCCACTAGGACATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGA 692

Qy         288 TTTCACTCTCACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCA 347
               ||||| |||||||||||||||| |||||||||||| ||||| |||||||||||| |||
Db         693 TTTCACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAATTTATTACTGTAAGCA 752

Qy         348 ATTTATAATACTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
               ||||||| ||||  |||||||   || |||| | || | | ||||
Db         753 ATTTATACTCTTCGGCACGTTCGGTGGAGGCACCAAGCTGGAGATCAAA 801


RESULT 13
US-09-423-439-37
; Sequence 37, Application US/09423439
; Patent No. 6390670
;   GENERAL INFORMATION:
;        APPLICANT: EMERY, Stephen Charles
;                   BLAKEY, David Charles
;        TITLE OF INVENTION: CHEMICAL COMPOUNDS
;        NUMBER OF SEQUENCES: 60
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Winthrop, L.L.P.
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/423,439
;             FILING DATE: 04-Nov-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB98/01294
;             FILING DATE: 05-MAY-1998
;             APPLICATION NUMBER: GB 9709421.5
;             FILING DATE: 10-MAY-1997
```

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;  INFORMATION FOR SEQ ID NO: 87;
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 2025 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: other nucleic acid
;    SEQUENCE DESCRIPTION: SEQ ID NO: 87;
US-09-429-430-87

  Query Match             98.8%;  Score 2720.6;  DB 4;  Length 2025;
  Best Local Similarity   99.0%;  Pred. No. 2.1e-77;
  Matches  800;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          48 TGGCACCTGTGGGGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCCTAGG 107
               ||||| ||||   ||||||| ||| ||||||||||   |||||||||| |||||||||
Db         456 TGGCGGCGGATCTGACATTGAGCTCTCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGG 515

Qy         108 AGAGACGGGCACTATTACTGCAAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAA 167
               |||||| || ||| || ||||||||||||||||||||||||||||||||| |||||||||| |
Db         516 AGAGAAGGTCACCATCAGCTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACCCGAAA 575

Qy         168 GAACTACTTGGCTTGTACCAGAGAAAGCAGGGCAGTCTCCTAAATGTGTGATCTACTG 227
               |||||||||||||||||||||||||||| |||||||||| |||||||||||||||||| ||
Db         576 GAACTACTTGCTTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAATGTGTTATCTATTG 635

Qy         228 GGCATCCGGGAATCCGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTC 287
               |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db         636 GGCATCCGTGATCCGGGGTCCCTGATCGCTTCATCGGCAGTGGATCTGGGACAGATTTC 695

Qy         288 TTCACTCTCACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAA 347
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         696 TTCACTCTCACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAA 755

Qy         348 ATCTATAAATCCTTATACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
               ||||||||| ||||   |||||||    || ||||| | || || ||||
Db         756 ATCTTATACTCTTCGGAGTTCGGGTGGAGGCACCAAGCTGGAGATCAAA 804


RESULT 14
US-09-929-856-188
; Sequence 188, Application US/09292856
; Patent No. 6194568
;  GENERAL INFORMATION:
;    APPLICANT:  Bratt, Andrew
;    APPLICANT:  Wong, Ellyl
;    TITLE OF INVENTION:  DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
;    TITLE OF INVENTION:  ROLLING TEMPLATES
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LERNER, DAVID, LITTENBERG, KRUMHOLZ &
;      ADDRESSEE:  MENTLIK
;      STREET:  600 South Avenue West
;      CITY:  Westfield
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07090
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/292,856
;      FILING DATE:  15-SEP-1999
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Foley, Shawn P.
;      REGISTRATION NUMBER:  43,071
;      REFERENCE/DOCKET NUMBER:  ROSE 4.0-007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 654 5000
;      TELEFAX:  908 654 7866

;  INFORMATION FOR SEQ ID NO:  188;
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  342 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..342
US-08-929-856-188

  Query Match             67.5%;  Score 267.2;  DB 3;  Length 342;
  Best Local Similarity   87.2%;  Pred. No. 1.4e-76;
  Matches  293;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          61 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCCTAGGAGAGACGGGCACT 120
               |||||||| || |||||||||||   ||||||||||       |||||||| || |||
Db           1 GACATTGTGATGTCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAAGGTCACC 60

Qy         121 ATTACTGCAAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 180
               || |||||||||||| | | ||||||||||||| |||||| |||||| ||||||
Db          61 ATCAGCTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACCCGAAAGAACTACTTGGCT 120

Qy         181 TGTACCAGCAGAAACCAGGGCAGTCTCCTAAATGTGTGATCTACTGGGCATCCGGGAATCC 240
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TGTACCAGCAGAAACCAGGGCAGTCTCCTAAATGTGTTATCTATTGGGCATCCGTGATCC 180

Qy         241 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 300
               |||||||||||||||||||||||||||   |||||||||||||||||||||||||||||
Db         181 GAATCTGGGGTCCCTGATCGCTTCATCGGCAGTGGATCTGGGACAGATTTCACTCTCACC 240

Qy         301 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAAATCTATAAATCCT 360
               |||||||||| |||||||||||||||||||||||||||||||||||    |||||||||
Db         241 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCATAATTCTTATAATCCT 300

Qy         361 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAA 396
                  |||||||     || |||||| |||||| |||
Db         301 CGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 336


RESULT 15
US-07-916-098A-54
; Sequence 54, Application US/07916098A
; Patent No. 5871732
;  GENERAL INFORMATION:
;    APPLICANT:  ISAKEY, LINDA C.
;    APPLICANT:  OBRIEN, PATRICIA L.
;    APPLICANT:  THOMAS, DAVID W.
;    APPLICANT:  ROSA, MARGARET D.
;    APPLICANT:  ROSA, JOSEPH J.
;    TITLE OF INVENTION:  ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALLEGRETTI & WITCOFF, LTD.
;      STREET:  10 SOUTH WACKER DRIVE
;      CITY:  CHICAGO
;      STATE:  ILLINOIS
;      COUNTRY:  U.S.A.
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/916,098A
;      FILING DATE:  July 24, 1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/08843
;      FILING DATE:  No. 587173ember 27, 1991
```

; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/918,542
; FILING DATE: No. 58/174,ember 27, 1990
; CLASSIFICATI N: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN L. MCDONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,81-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5817
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1701 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "pMDK1006 insert"
DS of 916 from 98A 54

Query Match 67.5%; Score 267.2; DB 2; Length 1701;
Best Local Similarity 81.0%; Pred. No. 2.4e-76;
Matches 411; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Qy          18 GAACAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGGGACATTGTGCTG 77
               || ||| | ||     | |||||||| ||| |  | ||  || | || || || ||  ||
Db          54 GTTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTGCCAGGTGCCAGATGTGATATCGTAATG 113

Qy          78 ACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACTATTAGCTGCAAA 137
               || |||||||||| ||||| |||||     | ||||||||||| ||||| | ||||||
Db         114 ACCCAGTCTCCAGACTCCCTAGCTGTGTCACTTGGAGAGAGGGCTACTATAAACTGCAAG 173

Qy         138 TCCAGTCAGAGTCTGTTCAACAGTAGAACCCGAGAAGAACTACTTGGCTTGGTACCAGCAG 197
               ||||| ||| || | | |||| | | | |||||||||||| ||||||||||
Db         174 TCTAGTGGGAGCCTTTTATATAGTACCAATCAAAAGAACTACTTGGCCTGGTACCAGCAG 233

Qy         198 AAACCAGGGCAGCCTCCTAAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTC 257
               |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         234 AAACCAGGGCAGCCTCCTAAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTC 293

Qy         258 CCTGATCGCTTCACAGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTG 317
               |||||| |||||  ||||||||||| |||||||||||||||||||||||||||||| ||
Db         294 CCTGATCGTTTCTCAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTTTG 353

Qy         318 CAGGCTGAAGACGTGGCAGTTTATTACTGCAGGCAATCTTATAATCTTTACACGTTCGGA 377
               |||||||||||||||||||||||||||    ||||| |||||     |   ||||||||
Db         354 CAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATAGCTATCCGACGTTCGGT 413

Qy         378 CAGGGGACCAAGGTGGAAATAAAA 401
               |  |||||||| |||| || ||||
Db         414 CAGAGGACCAAGCTGGAGATCAAA 437
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Search completed: June 17, 2003, 20:00:54
Job time : 35.618 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 14, 2003, 15:22:38 ; Search time 13.942 Seconds
(without alignments)
916.212 Million cell updates/sec

Title: US-09-249-011B-8
Perfect score: 681
Sequence: 1 MDSQAQVFIFLLLWVSGTCG YCTQSYNFYFFGQGTKVEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	596	87.5	133	2	PS0023	Ig kappa chain pre
2	558.5	82.0	134	1	K4HU17	Ig kappa chain pre
3	558	81.9	120	2	G33932	Ig kappa chain pre
4	553.5	81.3	134	2	S49541	anti-Sm antibody V
5	552	81.1	133	1	K4HUL1	Ig kappa chain pre
6	542.5	79.7	138	2	S26040	Ig kappa chain pre
7	541.5	79.5	145	2	PL0014	Ig kappa chain pre
8	539.5	79.2	134	2	PC1214	Ig kappa chain pre
9	538.5	79.0	135	2	S38807	Ig light chain V J
10	536	78.7	108	2	A53261	Ig kappa chain pre
11	535.5	78.6	129	2	S40347	Ig kappa chain - h
12	534.5	78.4	240	2	S06084	Ig kappa chain pre
13	528.5	77.6	132	2	S46873	Ig kappa chain V-J
14	525.5	77.1	134	2	S25917	Ig kappa chain V r
15	515	75.6	121	1	K4H0	Ig kappa chain pre
16	510	74.9	113	2	PT0407	Ig light chain V r
17	508.5	74.7	120	2	S53147	antibody light cha
18	506.5	74.4	124	2	S40364	Ig kappa chain - h
19	506	74.3	112	2	S43103	Ig kappa chain V-J
20	502.5	73.8	113	2	S34002	Ig kappa chain V r
21	500.5	73.5	136	2	A49137	Ig kappa chain pre
22	497.5	73.1	114	1	K4HULN	Ig kappa chain V-I
23	494	72.5	112	2	PL0265	Ig kappa chain V r
24	493.5	72.5	129	2	S40329	Ig kappa chain V-J
25	492	72.2	113	2	PT0408	Ig light chain V r
26	490.5	72.0	113	2	S30520	Ig kappa chain V r
27	482	70.8	112	2	S41393	Ig kappa chain V r
28	480	70.5	103	2	PH1047	Ig light chain V r
29	479.5	70.4	113	2	S34003	Ig kappa chain V r
30	475	69.8	103	2	PH1052	Ig light chain V r
31	474.5	69.7	111	2	S03303	Ig kappa chain V r
32	473.5	69.5	114	2	S44116	Ig kappa chain V-J
33	473.5	69.5	114	2	S44119	Ig kappa chain V-J
34	471	69.2	104	2	PH1101	Ig light chain V r
35	470.5	69.1	113	2	S30523	Ig kappa chain V r
36	470	69.0	104	2	PH1102	Ig light chain V r
37	467	68.6	103	2	PH1051	Ig light chain V r
38	466	68.4	104	2	PH1104	Ig light chain V r
39	464	68.1	103	2	PH1050	Ig light chain V r
40	462.5	67.9	113	2	PL0263	Ig kappa chain V r
41	460	67.5	101	2	PH1046	Ig light chain V r
42	457	67.1	104	2	PH1103	Ig light chain V r
43	452.5	66.4	113	2	PL0264	Ig kappa chain V r
44	452.5	66.4	214	2	S68212	Ig kappa chain (Ma
45	452	66.4	106	2	A49138	IgA kappa rheumato

ALIGNMENTS

RESULT 1
PS0023
Ig kappa chain precursor V region (6A4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: PS0023
R;Marquet, M.; Ecklardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Demaday, R.
Gene 74, 335-345, 1988
A;Title: Cloning and characterization of cDNAs coding for the heavy and light chains
A;Reference number: PS0023; MUID:89232725; PMID:3149944
A;Accession: PS0023
A;Molecule type: mRNA
A;Residues: 1-133 <MAR>
A;Experimental source: strain BALB/c
A;Note: the amino terminal four residues of the mature protein were directly sequence
C;Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aer
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-133/Product: Ig kappa chain V region 6A4 #status experimental <1GV>
F;36-116/Domain: immunoglobulin homology <1MM>

Query Match 87.5%; Score 596; DB 2; Length 133;
Best Local Similarity 86.4%; Pred. No. 1.3e-43;
Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 MDSQAQVFIFLLLWVSGTCGDIVLTQSPASLAVSLGERATISCRASESVEYYGTSLMQWYQQKP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDSQAQVFIFLLLWVSGTCGDIVLTQSPASLAVSLGERATISCRASESVEYYGTSLMQWYQQKP 60

Qy         61 GQPPKLLIYAASNVESGVPARFSGSGSGTDFSLNIHPVEEEDAATYYCQQSRKVPYTFGGGTK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GQPPKLLIYAASNVESGVPARFSGSGSGTDFSLNIHPVEEEDAATYYCQQSRKVPYTFGGGTK 120

Qy        121 LEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ 180

Qy        181 DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 228
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Db        181 DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 228
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RESULT 2
K4HU17
Ig kappa chain precursor V IV region (B17) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
C;Accession: A01905
R;Marsh, P.; Mills, F.; Gould, H.
Nucleic Acids Res. 13, 6531-6544, 1985
A;Title: Detection of a unique human Vkappa IV germline gene by a cloned cDNA probe.
A;Reference number: A01905; MUID:86041854; PMID:2997718
A;Accession: A01905
A;Molecule type: mRNA
A;Residues: 1-134 <MAR>

A;N
A;Notes: The sequence was determined from the differentiated gene
A;Notes: The authors translated the codon TGT for residue 7 as Trp
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
both disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG
F;21-144/Product: Ig kappa chain V IV region (JI) #status predicted <MAT
F;21-43/Region: framework 1
F;36-116/Domain: immunoglobulin homology <IMM
F;44-60/Region: complementarity determining 1
F;61-75/Region: framework 2
F;76-82/Region: complementarity determining 2
F;83-114/Region: framework 3
F;115-121/Region: complementarity determining 3
F;122-133/Region: framework 4
F;43-114/Disulfide bonds: #status predicted

Query Match 82.0%; Score 550.5; DB 1; Length 144;
Best Local Similarity 85.4%; Pred. No. 1.2e-40;
Matches 111; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

Qy 4 QAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRENYLAWYQ 63
Db 4 QIQVFISLLLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSILYSSDNKNYLAWYQ 63

Qy 64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNLYT 122
Db 64 QKPGQPPKLLIYCASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNLPWT 123

Qy 123 FGQGTKVEIK 132
Db 124 FGQGTKVEIK 133

RESULT 3
K03022
Ig kappa chain precursor V region (B23) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: A03022
R;Bernard, O.; Hozumi, N.; Tonegawa, S.; Acad. Sci. U.S.A. 86, 3745-3749, 1989
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ
A;Reference number: A03022; MUID:89282823; PMID:2497887
A;Accession: A03022
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-129 <BAT
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG

Query Match 81.0%; Score 550; DB 2; Length 129;
Best Local Similarity 88.8%; Pred. No. 1.2e-40;
Matches 104; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRENYLA 60
Db 1 MDCQAQVLILLLLWVSGTDGDIVMSQSPSSLAVSAGEKVTMSCKSSQSLLNSGNQKNYLA 60

Qy 61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNL 120
Db 61 WYQQKPKQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNL 120

RESULT 4
C14C41
mAb 30 antibody VL chain (V-kappa I/J-kappa 2) - mouse
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C;Accession: C14C41
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, J.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S48797
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <MAH
A;Cross-references: EMBL:...36347; NID:g560841; PIDN:CAA80466.1; PID:g560842
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-116/Domain: immunoglobulin homology <IMM

Query Match 81.1%; Score 552; DB 1; Length 134;
Best Local Similarity 83.7%; Pred. No. 6.8e-40;
Matches 108; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 4 QAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRENYLAWYQ 63
Db 4 QIQVFISLLLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSILYSSDNKNYLAWYQ 63

Qy 64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNLYT 123
Db 64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTAFT 123

Qy 124 FGQGTKVEIK 133
Db 124 FGPGTKVDIK 133

RESULT 5
K4BUJI
Ig kappa chain precursor V IV region (JI) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
C;Accession: A01904
R;Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H
Nucleic Acids Res. 14, 6515-6529, 1986
A;Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single ge
A;Reference number: A93589; MUID:86041854; PMID:2997712
A;Accession: A01904
A;Molecule type: DNA
A;Residues: 1-133 <KLO
A;Cross-references: GDB:119341; OMIM:146980
C;Genetics:
A;Gene: GDB:IGKV
A;Cross-references: GDB:119341; OMIM:146980
A;Map position: 2p12-2p12
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
both disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG
F;21-133/Product: Ig kappa chain V IV region (JI) #status predicted <MAT
F;21-43/Region: framework 1
F;36-116/Domain: immunoglobulin homology <IMM
F;44-60/Region: complementarity determining 1
F;61-75/Region: framework 2
F;76-82/Region: complementarity determining 2
F;83-114/Region: framework 3
F;115-122/Region: complementarity determining 3
F;123-133/Region: framework 4
F;43-114/Disulfide bonds: #status predicted

Query Match 81.1%; Score 552; DB 1; Length 133;
Best Local Similarity 83.7%; Pred. No. 6.8e-40;
Matches 108; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 4 QAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRENYLAWYQ 63
Db 4 QIQVFISLLLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSILYSSDNKNYLAWYQ 63

Qy 64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNLYTF 123

```
Db         64 QKFGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC[illegible] 123

Qy        124 GQGTKVEIK 132

Db        124 GGGTKVEIK 132


RESULT 6
S26040
Ig kappa chain precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jan-2000
C;Accession: S26040; S78098
R;Okamoto, M.; Honjo, T.
Nucleic Acids Res. 18, [illegible], 1990
A;Title: Nucleotide sequences of the gene/cDNA coding for anti murine erythrocyte autoan
A;Reference number: [illegible]; MUID:[illegible]; PMID:[illegible]
A;Accession: S26040
A;Molecule type: DNA
A;Residues: 1-138 <OKA>
A;Cross-references: EMBL:X51742
A;Note: the authors translated the codon AGC for residue 107 as Thr and AGT for residue
R;Okamoto, M.
submitted to the EMBL Data Library, February 1990
A;Reference number: S78098
A;Accession: S78098
A;Molecule type: DNA
A;Residues: 1-87,'W',89-138 <OKW>
A;Cross-references: EMBL:X51742; NID:g52697; PIDN:CAA36032.1; PID:g52698
C;Genetics:
A;Introns: 22/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-138/Product: Ig kappa chain (fragment) #status predicted <MAT>
F;41-121/Domain: immunoglobulin homology <IMM>

  Query Match             79.7%;  Score 542.5;  DB 2;  Length 138;
  Best Local Similarity   75.2%;  Pred. No. 4.5e-34;
  Matches  103;  Conservative   17;  Mismatches   12;  Indels    5;  Gaps    1;

Qy          1 MDSQAQVLILLLLWVSG-----TCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTR 55

Db          1 MESQAQVLMLLLLWVSGFKKKSTCGDIVMS[illegible] 60

Qy         56 [illegible] 115

Db         61 KNYLAWYQQK[illegible] 120

Qy        116 QS[illegible] 132

Db        121 QYYSFLLFGAGTKLELK 137


RESULT 7
PL0014
Ig kappa chain precursor V region (F6-3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0014
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0014
A;Molecule type: mRNA
A;Residues: 1-145 <CHE>
A;Experimental source: cell line F6-3
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcho
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-134/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F;[illegible]/Domain: immunoglobulin homology <IMM>
F;44-60/Region: complementarity-determining 1
F;76-82/Region: complementarity-determining 2
F;115-123/Region: complementarity-determining 3
F;135-145/Domain: constant region (fragment) #status predicted <COR>

  Query Match             79.5%;  Score 541.5;  DB 2;  Length 145;
  Best Local Similarity   77.6%;  Pred. No. 5.7e-39;
  Matches  104;  Conservative   18;  Mismatches    9;  Indels    3;  Gaps    [illegible];

Qy          1 MDSQAQVLILLLLWVS[illegible]NSRTRKNYLA 60

Db          1 [illegible]LYNQKNFLA 60

Qy         61 WYQQKP[illegible]YNL 120

Db         61 [illegible] 119

Qy        121 Y--[illegible]GTKVEIK 132

Db        120 YPLTFGSGTKLEMK 133


RESULT 8
PC1214
Ig kappa chain precursor V region (mAb H8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PC1214
R;Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.[illegible]; K
Gene 121, 331-335, 1992
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a
A;Reference number: PC1213; MUID:93077049; PMID:1446832
A;Accession: PC1214
A;Molecule type: mRNA
A;Residues: 1-134 <HON>
A;Cross-references: GB:M98042; NID:g196749; PIDN:AAA38777.1; PID:g196750
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-134/Product: Ig light chain V region #status predicted <MAT>
F;36-116/Domain: immunoglobulin homology <IMM>

  Query Match             [illegible];  Score [illegible];  DB 2;  Length 134;
  Best Local Similarity   78.9%;  Pred. No. 7.8e-39;
  Matches  [illegible];  Conservative   14;  Mismatches   [illegible];  Indels    1;  Gaps    1;

Qy          1 [illegible]NSRTRENYLA 60

Db          1 [illegible]ENYLA 60

Qy         61 WYQQKP[illegible]YNL 120

Db         61 WYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISNVKAEDLAVYYCQQYYNY 120

Qy        121  YTFGQGTKVEIK 132

Db        121 PSTFGGGTYLEIK 133


RESULT 9
S38807
Ig light chain V-J region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S38807
R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.
Immunogenetics 36, 15-21, 1992
A;Title: Molecular characterization of the variable regions of a mouse polyreactive [illegible]
A;Reference number: S38807; MUID:92267566; PMID:1587549
A;Accession: S38807
A;Status: preliminary
```

A;Molecule type: mRNA
A;Residues: 1-145 <SIG>
A;Cross-reference: EMBL:X60040
A;Note: the authors translated the codon GGT for residue 1 as Ala and GGC for residue 21
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-98/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 545.5; DB 2; Length 145;
Best Local Similarity 78.0%; Pred. No. 1.4e-48;
Matches 103; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

Qy 1 MEGLAVLILLAWVSGSCAEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ 60
MEGLAVLILLAWVSGSCAEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ
Db 1 MEGLAVLILLAWVSGSCAEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ 60

Qy 61 WYQQKPGQAPRLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
WYQQKPGQAPRLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL
Db 61 WYQQKPGQAPRLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120

Qy 121 YTFGQGTKVEI 131
YTFGQGTKVEI
Db 121 YTFGQGTKVEI 131

RESULT 10
A56261
Ig kappa chain precursor V-J-C region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C;Accession: A56261
R;Gaynes, M.; Proud'homme, J.L.; Bauwens, M.; Lombard, G.; Auvaurier, P.
J. Clin. Invest. 87, 2186-2190, 1991
A;Title: Structure of a monoclonal kappa chain of the VK IV subgroup in the kidney and p
A;Reference number: A56261; MUID:91250576; PMID:1904072
A;Accession: A56261
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-138 <Gay>
A;Cross-reference: GB:M38267
A;Note: authors translated the codon TTG for residue 12 as Phe
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-96/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 544; DB 2; Length 138;
Best Local Similarity 89.9%; Pred. No. 1.6e-48;
Matches 106; Conservative 7; Mismatches 10; Indels 2; Gaps 1;

Qy 4 QAQVELGLLLLWVSGSCGQIVLTQSPGSLAVSLGERATISCKASESVDSYGNSFMHWYQ 63
QAQVELGLLLLWVSGSCGQIVLTQSPGSLAVSLGERATISCKASESVDSYGNSFMHWYQ
Db 4 QAQVFISLLLWISGARGDIVMTQSPDSLAVSAGERATINCKSSQSVFFSSNNKNYLAWYQ 63

Qy 64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNL 123
QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNL
Db 64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTNFTLTISSLQAEDVAVYYCQQYYSTPLT 123

Qy 124 FGQGTKVEIK 133
FGQGTKVEIK
Db 124 FGQGTKVEIK 133

RESULT 11
S40647
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40647
R;Klein, R.; Raeuchen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 4238-4241, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40612; MUID:94080809; PMID:8297341
A;Accession: S40647
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
A;Cross-reference: EMBL:X72457; NID:g441382; PIDN:CAA51125.1; PID:g441383
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-98/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 545.5; DB 2; Length 129;
Best Local Similarity 81.4%; Pred. No. 1.6e-48;
Matches 105; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

Qy 1 MEGLAVLILLAWVSGSCAEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ 60
MEGLAVLILLAWVSGSCAEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ
Db 1 MEGLAVLILLAWVSGSCAEIVMTQSPSSLAVSAGETVTINCKSSQSLFYSGNQKNYLAWYQ 60

Qy 61 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNL 120
QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNL
Db 61 QKPGQPPKLLIYWASTRQSGVPDRFIGSGSGTDFTLTISSVQAEDLAIYYCLQYYEI 120

Qy 121 YTFGQGTKVEIK 132
YTFGQGTKVEIK
Db 121 YTFGAGTKLELK 132

RESULT 12
S06084
Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of V3 Ar 1.2.3 rat myeloma immunoglobulin kappa chain c
A;Reference number: S06084; MUID:90016888; PMID:2508067
A;Accession: S06084
A;Molecule type: mRNA
A;Residues: 1-240 <Cro>
A;Cross-reference: EMBL:X16129, NID:g56457, PIDN:CAA34256.1; PID:g56458
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 542.5; DB 2; Length 240;
Best Local Similarity 75.9%; Pred. No. 5.4e-48;
Matches 101; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

Qy 1 MEGLAVLILLAWVSGSCAEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ 60
MEGLAVLILLAWVSGSCAEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ
Db 1 MESQTLVFVSILLWLSGTDGDIVMTQSPSSLAVSAGFTVTINCKSSQSLFYSGNQKNYLA 60

Qy 61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNL 120
WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDLAIYYCLQYYEI
Db 61 WYQQKPGQSPKLLIYWASTRQSGVPDRFIGSGSGTDFTLTISSVQAEDLAIYYCLQYYEI 120

Qy 121 YTFGQGTKVEIK 132
YTFGAGTKLELK
Db 121 FTFGSGSKLEIK 133

RESULT 13
S46373
Ig kappa chain V-J region (124 G) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46373; S38647
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene
A;Reference number: S46369; MUID:94319375; PMID:8039491
A;Accession: S46373

A;Molecule type: mRNA
A;Residues: 1-132 <BEN>
A;Cross-references: EMBL:Z27174; NID:g415963; PIDN:CAA81698.1; PID:g415964
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-114/Domain: immunoglobulin homology <IMM>

Query Match 27.6%; Score 528.5; DB 2; Length 172;
Best Local Similarity 79.2%; Pred. No. 6.5e-38;
Matches 114; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

Qy 4 QAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLAWYQ 63
Db 2 QTQVFISLLIWISGAYGDIVMTQSPSTLAVTPGEPATINCKSSQSLVHSNGNTYLAWYL 61

Qy 64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 122
Db 62 QKPGQPPELLIHWASSRESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCHQYYSYPL 121

Qy 123 FGQGTKVEIK 132
Db 122 FGGGTKVDIK 131

RESULT 14
S21917
Ig kappa chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S21917
R;Mietaen, E.; Tuuse, A.; Knoppers, R.; Michels, M.; Maqeed, R.A.; Jefferis, R.; Gorth, F
submitted to the EMBL Data Library, July 1991
A;Description: A Human monoclonal IgA rheumatoid factor using the VK(IV) light chain gen
A;Reference number: S21916
A;Accession: S21917
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <MIE>
A;Cross-references: EMBL:X61125; NID:g33288; PIDN:CAA43437.1; PID:g33289
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-116/Domain: immunoglobulin homology <IMM>

Query Match 25.7%; Score 515.5; DB 2; Length 134;
Best Local Similarity 76.0%; Pred. No. 8.3e-37;
Matches 98; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

Qy 4 QAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLAWYQ 63
Db 4 QTQVFISLLIWISGAYGDIVMTQSPSTLAVTPGEPATINCKSSQSLVHSNGNTYLAWFQ 63

Qy 64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLYT 123
Db 64 QNPGQAPRLLIYWASARESGVPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYEDFPYT 123

Qy 124 FGQGTKVEI 131
Db 124 FGQGTKLEI 132

RESULT 15
K1HU
Ig kappa chain precursor V IV region - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
C;Accession: A01992
R;Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Meerkat, R.; Pohlenz, H.D.; Zachau, H.G.
Nucleic Acids Res. 13, 6515-6529, 1985
A;Title: Subgroup IV of human immunoglobulin K light chains is encoded by a single germl
A;Reference number: A93589; MUID:86041853; PMID:2997712
A;Accession: A01992
A;Molecule type: DNA
A;Residues: 1-121 <KLO>
A;Note: the sequence was determined from the germline gene
A;Note: there is only one Ig kappa V IV gene
C;Genetics:
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light c
Both disulfide bonds. In some cases, such as IgA and IgM, the subunits associate to
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-121/Product: Ig kappa chain precursor V-IV region #status predicted <MAT>
F;21-43/Region: framework 1
F;36-116/Domain: immunoglobulin homology <IMM>
F;44-60/Region: complementarity-determining 1
F;61-75/Region: framework 2
F;76-82/Region: complementarity-determining 2
F;83-114/Region: framework 3
F;115-121/Region: complementarity determining 3
C;4; 14disulfide bonds. #status predicted

Query Match 25.6%; Score 515; DB 1; Length 121;
Best Local Similarity 85.4%; Pred. No. 8.3e-37;
Matches 99; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 4 QAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLAWYQ 63
Db 4 QTQVFISLLIWISGAYGDIVMTQSPSTLSVSAGERATLNCKSSQSVVYSSNNRNYLAWYQ 63

Qy 64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYN 119
Db 64 QKPGQAPKLLIYWASTRESGVPDRFSGSGSGSDFTLTISSLQAEDVAVYYCQQYYS 119

Search completed: June 14, 2003, 15:08:13
Job time : 14.8427 secs

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SW protein : protein search, using sw model

Run on: June 14, 2003, 15:02:48 ; Search time 13.8127 Seconds
(without alignments)
556.506 Million cell updates/sec

Title: US-09-249-011B-8
Perfect score: 981
Sequence: 1 MLSLAVLILLLLNVSSSG.....YSLYSTNLTTEGLAIKVEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	571.5	84.9	134	1	KV4C_HUMAN	P06314 homo sapien
2	552	81.1	138	1	KV4B_HUMAN	P06313 homo sapien
3	515	75.6	121	1	KV40_HUMAN	P04212 homo sapien
4	502.5	74.8	114	1	KV4A_HUMAN	P01625 homo sapien
5	446	65.5	129	1	KV3H_HUMAN	P04207 homo sapien
6	442	64.9	129	1	KV3L_HUMAN	P18135 homo sapien
7	441	64.6	129	1	KV3M_HUMAN	P04206 homo sapien
8	418	61.4	133	1	KV2F_HUMAN	P06310 homo sapien
9	416.5	61.2	129	1	KV1W_HUMAN	P04431 homo sapien
10	409.5	60.1	128	1	KV3E_HUMAN	P04211 homo sapien
11	408.5	60.0	131	1	KV31_MOUSE	P01661 mus musculu
12	408.5	60.0	132	1	KV3F_MOUSE	P01658 mus musculu
13	396	58.1	115	1	KV31_HUMAN	P04433 homo sapien
14	394.5	57.9	116	1	KV3J_HUMAN	P04434 homo sapien
15	394	57.9	110	1	KV3P_MOUSE	P01668 mus musculu
16	388.5	57.0	136	1	KV5B_MOUSE	P01634 mus musculu
17	387.5	57.6	149	1	KV5A_MOUSE	P01633 mus musculu
18	384	56.4	109	1	KV3R_HUMAN	P01628 homo sapien
19	384	56.4	109	1	KV3F_HUMAN	P01624 homo sapien
20	383	56.2	109	1	KV3D_HUMAN	P01622 homo sapien
21	382.5	56.2	111	1	KV3B_MOUSE	P01665 mus musculu
22	382.5	56.2	111	1	KV3O_MOUSE	P01667 mus musculu
23	381	55.9	109	1	KV3E_HUMAN	P01623 homo sapien
24	381	55.9	117	1	KV2E_HUMAN	P06309 homo sapien
25	380.5	55.9	108	1	KV1M_HUMAN	P01605 homo sapien
26	380.5	55.9	111	1	KV3L_MOUSE	P01664 mus musculu
27	379.5	55.7	111	1	KV3U_MOUSE	P01673 mus musculu
28	377.5	55.4	111	1	KV3H_MOUSE	P01666 mus musculu
29	375.5	55.1	111	1	KV3N_MOUSE	P01676 mus musculu
30	374.5	55.0	111	1	KV3Q_MOUSE	P01669 mus musculu
31	374.5	55.0	111	1	KV3R_MOUSE	P01670 mus musculu
32	374.5	55.0	111	1	KV3S_MOUSE	P01671 mus musculu
33	373.5	54.8	115	1	KV2A_HUMAN	P01614 homo sapien
34	370	54.3	109	1	KV3G_HUMAN	P04209 homo sapien
35	368.5	54.1	117	1	KV1J_HUMAN	P01602 homo sapien
36	368.5	54.1	129	1	KV1X_HUMAN	P04432 homo sapien
37	367	53.9	108	1	KV3A_HUMAN	P01619 homo sapien
38	366.5	53.8	108	1	KV1V_HUMAN	P04430 homo sapien
39	366.5	53.8	111	1	KV3D_MOUSE	P01677 mus musculu
40	366.5	53.8	111	1	KV3J_MOUSE	P01662 mus musculu
41	366.5	53.8	111	1	KV31_MOUSE	P01672 mus musculu
42	366.5	53.8	114	1	KV1A_MOUSE	P01632 mus musculu
43	365.5	53.7	109	1	KV1H_HUMAN	P01609 homo sapien
44	362.5	53.2	111	1	KV3C_MOUSE	P01656 mus musculu
45	362	53.2	113	1	KV2B_HUMAN	P01615 homo sapien

ALIGNMENTS

RESULT 1
KV4C_HUMAN
ID KV4C_HUMAN STANDARD; PRT: 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1990 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig Kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041784; PubMed=2997715;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe.";
RL Nucleic Acids Res. 13:6541-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT 1986) to the EMBL/GenBank/DDBJ databases.
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CC or send an email to license@isb-sib.ch).
DR EMBL; X-----; CAA25733.1; -.
DR PIR; A01905; K4HU17.
DR HSSP; P00626; 1WIE.
DR InterPro; IPR003596; Ig_MHC.
DR InterPro; IPR003599; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 59 COMPLEMENTARITY DETERMINING 1.
FT DOMAIN 60 75 FRAMEWORK 2.
FT DOMAIN 76 92 COMPLEMENTARITY DETERMINING 2.
FT DOMAIN 93 114 FRAMEWORK 3.
FT DOMAIN 115 121 COMPLEMENTARITY DETERMINING 3.
FT DOMAIN 122 133 FRAMEWORK 4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 13566 MW; 6413A2FF [illegible] CRC64;

Query Match 84.9%; Score 571.5; DB 1; Length 134;
Best Local Similarity 86.2%; Pred. No. 5.4e-52;
Matches 112; Conservative 0; Mismatches 11; Indels 1; Gaps 1;



RESULT 2
KV4B_HUMAN
ID KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -!- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
CC ---------- ----- ---------- ---------- -- ----- --------
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CC
DR EMBL; Z00022; CAA77318.1; -.
DR PIR; A01902; K4HUIL.
DR HSSP; P01834; 1WIL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 60 COMPLEMENTARITY DETERMINING 1.
FT DOMAIN 61 75 FRAMEWORK 2.
FT DOMAIN 76 82 COMPLEMENTARITY DETERMINING 2.
FT DOMAIN 83 114 FRAMEWORK 3.
FT DOMAIN 115 122 COMPLEMENTARITY DETERMINING 3.
FT DOMAIN 123 132 FRAMEWORK 4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 9FB9536006744AB4 CRC64;

Query Match 91.7%; Score 552; DB 1; Length 133;
Best Local Similarity 83.7%; Pred. No. 5.5e-50;
Matches 109; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

RESULT 3
KV40_HUMAN
ID KV40_HUMAN STANDARD; PRT; 121 AA.
AC P06412;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -!- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
CC ---------- ----- ---------- ---------- -- ----- --------
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CC
DR EMBL; Z00023; CAA77318.1; -.
DR PIR; A01902; K4HU.
DR HSSP; P01834; 1WIL.
DR Genew; HGNC:5834; IGKV4-1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD418BD33974 CRC64;

Query Match 75.6%; Score 515; DB 1; Length 121;
Best Local Similarity 85.9%; Pred. No. 3.2e-46;
Matches 99; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

RESULT 4

```
KV1A_HUMAN
ID   KV1A_HUMAN     STANDARD;      PRT;   114 AA.
AC   P01625;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-IV region Len.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76004342; PubMed=50995;
RA   Schneider M., Hilschmann N.;
RT   "The primary structure of a monoclonic immunoglobulin L chain of
RT   subgroup IV (of the kappa type (Bence-Jones protein Len).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN   [2]
RP   REVISION OF 9.
RA   Salmon A.;
RL   Submitted (AUG-1996) to the SWISS-PROT data bank.
CC   -!- MISCELLANEOUS: THE 3' PART OF THIS CHAIN HAS THE INV (1) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A02003; K4HUEN.
DR   HSSP; P01834; 1BEL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK-1.
FT   DOMAIN       24     40       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN       41     55       FRAMEWORK-2.
FT   DOMAIN       56     62       COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN       63     94       FRAMEWORK-3.
FT   DOMAIN       95    101       COMPLEMENTARITY DETERMINING 3.
FT   DOMAIN      102    113       FRAMEWORK-4.
FT   DISULFID     23     94       BY SIMILARITY.
FT   NON_TER     114    114
SQ   SEQUENCE   114 AA;  12640 MW;  9647FED17F226495 CRC64;

  Query Match             75.9%;  Score 546;  DB 1;  Length 114;
  Best Local Similarity   86.7%;  Prod. No. 5.7e-44;
  Matches   98;  Conservative    7;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          21 DIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLA 62
               |:|:|||||||||||||||||||||||:| |  :|||||||||||||||||||||||
Db           1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAW 42

Qy          63 WYQQKPGQPPKLLIYWAS TRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGQGTKLEIK 132
               |:|||||||||||||||| | ||  :|||||||||||||||||||||||||||||||||||||||||||||
Db          43 WFQQKPGQSPKLLIYGAS TRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQQYYSTPFTFGSGTKLEMK 112

Qy         133 EYIFQQTIKVEIK 145
              :|||||||:||||
Db         113 EWIFPPSVKVEIK 125


RESULT 5
KV4B_HUMAN
ID   KV4B_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04209;
DT   20-MAR-1987 (Rel. 04, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region CLL precursor (Rheumatoid factor)
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86177570; PubMed=6083417;
RA   Klein F.R., Scope T., Pons S., Beltramini L.G., Ford J.J., Olson P.D.,
RA   Goldfien R., Carson D.A.;
RT   "Cloning and sequence determination of a human rheumatoid factor
RT   light chain gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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CC   or send an email to license@isb-sib.ch).
DR   EMBL; M12748; AAA59092.1; -.
DR   PIR; A01898; K4HUCL.
DR   HSSP; P01834; 1WEL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    129       Ig KAPPA CHAIN V-III REGION CLL.
FT   DOMAIN       21     44       FRAMEWORK 1.
FT   DOMAIN       45     54       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN       55     69       FRAMEWORK 2.
FT   DOMAIN       70     76       COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN       77    108       FRAMEWORK 3.
FT   DOMAIN      109    119       COMPLEMENTARITY DETERMINING 3.
FT   DOMAIN      120    129       JK1 SEGMENT.
FT   DISULFID     43    108       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14275 MW;  5C13B411BE606C14 CRC64;

  Query Match             65.5%;  Score 446;  DB 1;  Length 129;
  Best Local Similarity   66.7%;  Prod. No. 4.3e-39;
  Matches   90;  Conservative   20;  Mismatches   15;  Indels   10;  Gaps    3;

Qy          1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLA 60
              ||: |||| ||||||  | |||||||| ||||| |||||||||||||||||||||||||
Db          1 MEAIAQDLTLVLLWVFIIGGEIVMTQSPATLSVSPGERATLSCRASQSVSNN------LA 54

Qy         61 WYQQKPGQPPKLLIYWAS TRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGQ 124
              |||||||||||||||||| | ||  :|||||||||||||||||||||||||||||||||||||||
Db         55 WFQQKPGQAPRLLIYGAS TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPAFGQ 118

Qy        125 GTKVEIK 132
             |||||||
Db        119 GTKLEIK 125


RESULT 6
KV3L_HUMAN
ID   KV3L_HUMAN     STANDARD;      PRT;   129 AA.
AC   P01845;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HAH precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171127; PubMed=3127523;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC       AUTOANTIBODIES EXPRESSED IN PATIENTS WITH "HAIRY-CELL" LYMPHOCYTIC
CC       LEUKEMIA.
DR   PIR; P16622; K4HUHA.
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DR   HSSP; P06312; 1WEL.
DR   InterPro; IPR003599; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   PFam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    129       IG KAPPA CHAIN V III REGION HAH.
FT   DOMAIN      21     43       FRAMEWORK 1.
FT   DOMAIN      44     55       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN      56     70       FRAMEWORK 2.
FT   DOMAIN      71     77       COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN      78    109       FRAMEWORK 3.
FT   DOMAIN     110    118       COMPLEMENTARITY DETERMINING 3.
FT   DOMAIN     119    129       JK1 SEGMENT.
FT   DISULFID    43    109       BY SIMILARITY.
FT   NON_TER    129    129
SQ   SEQUENCE   129 AA;  14073 MW;  D3059292772774D0 CRC64;

  Query Match             64.9%;  Score 442;  DB 1;  Length 129;
  Best Local Similarity   96.9%;  Pred. No. 1.8e-98;
  Matches   89;  Conservative   19;  Mismatches   19;  Indels    6;  Gaps    2;

Qy          1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLA 60
              |:: |:|:| ||||||:  | |:|||||||:|:|:| ||||||:|:|||:|:|||:|:|     |||
Db          1 MEIPAQLLFLLLLWLPGIRGEIVLTQSPGTLSLSPGERATLSCRASQSVSSS--YLA 55

Qy         61 WYQQKPGQAPRLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQ SYN 119
              |||||||:|:|||| |:|:| :|:|||||||||||||||:||| |:|| |:|||| |  :
Db         56 WYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS 115

Qy        120 LYIFGQGIKVEIK 132
              |||||:|||||
Db        116 PWIFGQGIKVEIK 128


RESULT 7
KV3M_HUMAN
ID   KV3M_HUMAN     STANDARD;      PRT:   129 AA.
AC   P01836;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HIC precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041852; PubMed=2997711;
RA   Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT   "Human immunoglobulin kappa light chain genes of subgroups II and
RT   III.";
RL   Nucleic Acids Res. 13:6499-6513(1985).
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CC   or send an email to license@isb-sib.ch).
CC   -!- -!- -!- -!- -!-
DR   EMBL; Z00020; CAA77315.1;  -.
DR   PIR; A01890; K2HUKP.
DR   HSSP; P06312; 1WEL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   PFam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    129       IG KAPPA CHAIN V-III REGION HIC.
FT   DOMAIN      21     43       FRAMEWORK 1.
FT   DOMAIN      44     55       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN      56     70       FRAMEWORK 2.
FT   DOMAIN      71     77       COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN      78    109       FRAMEWORK 3.
FT   DOMAIN     110    118       COMPLEMENTARITY DETERMINING 3.
FT   DOMAIN     119    129       JK1 SEGMENT.
FT   DISULFID    43    109       BY SIMILARITY.
FT   NON_TER    129    129
SQ   SEQUENCE   129 AA;  14070 MW;  7395528EA2B87416 CRC64;

  Query Match             64.6%;  Score 440;  DB 1;  Length 129;
  Best Local Similarity   96.2%;  Pred. No. 1.8e-98;
  Matches   88;  Conservative   20;  Mismatches   19;  Indels    6;  Gaps    2;

Qy          1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLA 60
              |:: |:|:| ||||||:  | |:|||||||:|:|:| ||||||:|:|||:|:|||:|:|     |||
Db          1 MLTIAQLLFLLLLWLPGIRGEIVLTQSPGTLSLSPGERATLSCRASQSVSSS--YLA 55

Qy         61 WYQQKPGQAPRLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQ SYN 119
              |||||||:|:|||| |:|:| :|:|||||||||||||||:||| |:|| |:|||| |  :
Db         56 WYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTS 115

Qy        120 LYIFGQGIKVEIK 132
              |||||:|||||
Db        116 PWIFGQGIKVEIK 128


RESULT 8
KV2F_HUMAN
ID   KV2F_HUMAN     STANDARD;      PRT:   133 AA.
AC   P06310;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-II region RPMI 6410 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041852; PubMed=2997711;
RA   Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT   "Human immunoglobulin kappa light chain genes of subgroups II and
RT   III.";
RL   Nucleic Acids Res. 13:6499-6513(1985).
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CC   or send an email to license@isb-sib.ch).
CC   -!- -!- -!- -!- -!-
DR   EMBL; Z00020; CAA77315.1;  -.
DR   PIR; A01890; K2HUKP.
DR   HSSP; P06312; 1WEL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   PFam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    133       IG KAPPA CHAIN V-II REGION RPMI 6410.
FT   DOMAIN      21     43       FRAMEWORK 1.
FT   DOMAIN      44     59       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN      60     74       FRAMEWORK 2.
FT   DOMAIN      75     81       COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN      82    113       FRAMEWORK-3.
FT   DOMAIN     114    122       COMPLEMENTARITY DETERMINING 3.
FT   DOMAIN     123    132       FRAMEWORK-4.
FT   DISULFID    43    113       BY SIMILARITY.
FT   NON_TER    133    133
SQ   SEQUENCE   133 AA;  14707 MW;  5130CAF3C7A09EE CRC64;

  Query Match             61.4%;  Score 418;  DB 1;  Length 133;
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  Best Local Similarity   65.9%;  Pred. No. 3.4e-36;
  Matches   85;  Conservative   19;  Mismatches   23;  Indels    2;  Gaps    2;

Qy          5 AQVLTQLTSLILSASVGDRVTITCRASQSISSYLNWYQQ 64
              ||:  |:|||  |: |:|:|||| || |:||: |:|||:|||||: |      || |:||
Db          5 AQSGTQLMLWVFGSSGDVVMTQSPLSLPVILGQPASISCKSSQSLVYS-DGNIYLNWFQQ 63

Qy         65 KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLYTF 123
              :|| |: |||  | |:|||||||:|||||||| || :||:|| |||| | ::  :||
Db         64 KPGQSPQLLIYEVSNRDSGVPDRFSGSGSDTDFTLKISRVEAEDVGVYYCMQGTHWSWTF 123

Qy        124 GQGTKVEIK 132
              ||||:|:|
Db        124 GQGTKVEIK 132


RESULT 9
KV1W_HUMAN
ID   KV1W_HUMAN     STANDARD;      PRT:   129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Walker precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85214148; PubMed=6091043;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucl. Acids Res. 12:6027-6038(1984).
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; X03065; CAA26477.1; ALT_TERM.
DR   PIR; A01883; K1HUWK.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION WAL.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    119       COMPLEMENTARITY DETERMINING 3.
FT   DOMAIN      120    129       FRAMEWORK 4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;

  Query Match          61.2%;  Score 416.5;  DB 1;  Length 129;
  Best Local Similarity   65.9%;  Pred. No. 4.7e-36;
  Matches   85;  Conservative   16;  Mismatches   21;  Indels    7;  Gaps    2;

Qy          5 AQVLTQLTSLILSASVGDRVTITCRASQSISSYLNWYQQ 64
              ||:| |||||: |  :| :|||| || |:|:| ||:|:|||:      ||| ||||
Db          7 AQLLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSI  -   SNYLNWYQQ 60

Qy         65 KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLYTF 123
              |:| |||||  || :||| :|:|||||||||||||||||| || |:||:|||| |||| | ::
Db         61 KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLTF 120

Qy        124 GQGTKVEIK 132
              ||||:|:||
Db        121 GQGTRLEIK 129


RESULT 10
KV3K_HUMAN
ID   KV3K_HUMAN     STANDARD;      PRT:   128 AA.
AC   P06673;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region IARC/BL41 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86011852; PubMed=2997711;
RA   Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT   "Human immunoglobulin kappa light chain genes of subgroups II and
RT   III.";
RL   Nucleic Acids Res. 13:6499-6513(1985).
CC   -!- ---------- ---------- ---------- ---------- ---------- ----------
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CC   or send an email to license@isb-sib.ch).
CC   ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; Z00021; CAA77316.1; -.
DR   PIR; A01899; K3HU41.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    128       IG KAPPA CHAIN V-III REGION IARC/BL41.
FT   DOMAIN       21     43       FRAMEWORK 1.
FT   DOMAIN       44     54       COMPLEMENTARITY DETERMINING-1.
FT   DOMAIN       55     69       FRAMEWORK 2.
FT   DOMAIN       70     76       COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN       77    109       FRAMEWORK-3.
FT   DOMAIN      110    117       COMPLEMENTARITY DETERMINING 3.
FT   DOMAIN      118    128       JOINING SEGMENT.
FT   DISULFID     44    108       BY SIMILARITY.
FT   NON_TER     128    128
SQ   SEQUENCE   128 AA;  14070 MW;  CC8957F0FE0B9012 CRC64;

  Query Match          60.1%;  Score 409.5;  DB 1;  Length 128;
  Best Local Similarity   63.2%;  Pred. No. 2.5e-35;
  Matches   84;  Conservative   27;  Mismatches   21;  Indels    7;  Gaps    2;

Qy          1 MDSQAQVLTQLTSLILSASVGDRVTITCRASQSISSYLNWYQQ 64
              |:: ||:| ||||:  | |:|||||| :|:|: || ||:||:|||: ::      ||
Db          1 METPAQLLFLLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSN      TA 54

Qy         65 KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLYTF 123
              ||||| || |:||  ||:| :|:|||||||||||||||| || |: || |||| | ::
Db         55 KPGQAPRLLIHDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSYSTLTF 114

Qy        124 GQGTKVEIK 132
              ||||:|:||
Db        115 GPGTKLEIK 123
```

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RESULT 11
KV4I_MOUSE
ID   KV4I_MOUSE     STANDARD;      PRT:   131 AA.
AC   P01661;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region MOPC 63 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=78235887; PubMed=98179;
RA   Bernstein Y., Schechter I.;
RT   "Primary structures of N-terminal extra peptide segments linked to
RT   the variable and constant regions of immunoglobulin light chain
RT   precursors: implications on the organization and controlled
RT   expression of immunoglobulin genes.";
RL   Biochemistry 17:2392-2400(1978).
RN   [2]
RP   SEQUENCE OF 21-131.
RX   MEDLINE=73110225; PubMed=4691417;
RA   McKean D.J., Potter M., Hood L.E.;
RT   "Mouse immunoglobulin chains. Pattern of sequence variation among
RT   kappa chains with limited sequence differences.";
RL   Biochemistry 12:760-771(1973).
RN   [3]
RP   REVISIONS.
RX   MEDLINE=77012520; PubMed=99744;
RA   McKean D.J., Bell M., Potter M.;
RT   "Mechanisms of antibody diversity. Multiple genes encode structurally
RT   related mouse kappa variable regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:3914-3917(1977).
DR   PIR; A01933; KVMS3M6.
DR   HSSP; P01679; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence Jones protein; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    131       Ig KAPPA CHAIN V-III REGION MOPC 63.
FT   DOMAIN      21     44       FRAMEWORK 1.
FT   DOMAIN      44     58       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN      59     74       FRAMEWORK 2.
FT   DOMAIN      74     88       COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN      89    122       FRAMEWORK 3.
FT   DOMAIN     123    131       COMPLEMENTARITY DETERMINING 3.
FT   DISULFID    44    122       BY SIMILARITY.
FT   NON_TER    131    131
SQ   SEQUENCE   131 AA;  14291 MW;  E2E3E7F0B6B999CA CRC64;

  Query Match             60.0%;  Score 408.5;  DB 1;  Length 131;
  Best Local Similarity   62.4%;  Pred. No. 4.2e-45;
  Matches   84;  Conservative   21;  Mismatches   24;  Indels    2;  Gaps    2;

Qy          1 MDSQAQVLILLLLWVSGTCGDIVLTQSPASLAVSLGQRATISCKSSQSLLNSRTRKNYLA 60
              ||:   :| :|||||  |: ||||||||| |||||||:|||||||:|:|:  :    :||
Db          1 MEIIILFLLWVLLLWVF-GCCGDIVLTQSPASLAVSLGQRATISCRASKSV--NIYMNSFMH 58

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLPT 120
              |||:|:|||||||| ||  |||:| |||||| |||||| |:|||||  :|:|||| |:|| :
Db         59 WYQLKPGQSPKLLIYGASNLESGVPARFSGSGSGTDFSLNIHPVEEVDAATYYCQQSRKVPW 118

Qy        121 TFGGGTKLEIK 131
             ||| |||||||
Db        119 TFGSGTKLEIK 129


RESULT 12
KV3F_MOUSE
ID   KV3F_MOUSE     STANDARD;      PRT:   132 AA.
AC   P01658;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region MOPC 321 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE OF 1-37.
RX   MEDLINE=78235887; PubMed=98179;
RA   Bernstein Y., Schechter I.;
RT   "Primary structures of N-terminal extra peptide segments linked to
RT   the variable and constant regions of immunoglobulin light chain
RT   precursors: implications on the organization and controlled
RT   expression of immunoglobulin genes.";
RL   Biochemistry 17:2392-2400(1978).
RN   [2]
RP   SEQUENCE OF 21-132.
RX   MEDLINE=73110224; PubMed=4120629;
RA   McKean D.J., Potter M., Hood L.E.;
RT   "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT   chain.";
RL   Biochemistry 12:749-759(1973).
CC   -!- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C-REGION OF THIS
CC       BENCE-JONES PROTEIN WAS ALSO DETERMINED; IT DIFFERS FROM THAT
CC       REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC       RESIDUES.
DR   PIR; A01933; KVMS32.
DR   HSSP; P01679; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence Jones protein; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    132       Ig KAPPA CHAIN V-III REGION MOPC 321.
FT   DOMAIN      21     44       FRAMEWORK 1.
FT   DOMAIN      44     58       COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN      59     74       FRAMEWORK 2.
FT   DOMAIN      74     88       COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN      89    122       FRAMEWORK 3.
FT   DOMAIN     123    131       COMPLEMENTARITY DETERMINING 3.
FT   DOMAIN     132    132       FRAMEWORK 4.
FT   DISULFID    44    122       BY SIMILARITY.
FT   NON_TER    132    132
SQ   SEQUENCE   132 AA;  13527 MW;  9F2B859B0C22FBE9 CRC64;

  Query Match             60.0%;  Score 408.5;  DB 1;  Length 132;
  Best Local Similarity   58.6%;  Pred. No. 4.2e-45;
  Matches   78;  Conservative   28;  Mismatches   24;  Indels    2;  Gaps    2;

Qy          1 MDSQAQVLILLLLWVSGTCGDIVLTQSPASLAVSLGQRATISCKSSQSLLNSRTRKNYLA 60
              |:   :| :|||||  |: ||||||||| |||||||:|||||||:|:|:  :    :||
Db          1 MEIIILFLLWVLLLWVF-GCCGDIVLTQSPASLAVSLGQRATISCRASKSV--NIYMNSFMH 58

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLPT 120
              |||:|:|||||||| ||  |||:| |||||| |||||| |:|||||  :|:|||| |:|| :
Db         59 WYQLKPGQSPKLLIYGASNLESGVPARFSGSGSGTDFSLNIHPVEEVDAATYYCQQSRKVPW 118

Qy        121 TFGGGTKLEIK 131
             ||| |||||||
Db        119 TFGSGTKLEIK 129


RESULT 13
KV4I_HUMAN
ID   KV4I_HUMAN     STANDARD;      PRT:   115 AA.
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AC   P04434;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region VG precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87088282; PubMed=6440122;
RA   Pech M., Zachau H.G.;
RT   "Immunoglobulin genes of different subgroups are interdigitated
RT   within the VK locus.";
RL   Nucleic Acids Res. 12:9229-9236(1984).
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CC   ---------- ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; X01668; -; NOT_ANNOTATED_CDS.
DR   PIR; A01900; KVHUVG.
DR   HSSP; P06326; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    115       IG KAPPA CHAIN V-III REGION VG.
FT   DOMAIN      21     43       FRAMEWORK-1.
FT   DOMAIN      44     54       COMPLEMENTARITY DETERMINING-1.
FT   DOMAIN      55     69       FRAMEWORK-2.
FT   DOMAIN      70     76       COMPLEMENTARITY DETERMINING-2.
FT   DOMAIN      77    108       FRAMEWORK-3.
FT   DOMAIN     109    115       COMPLEMENTARITY DETERMINING-3.
FT   DISULFID    43    108       BY SIMILARITY.
FT   NON_TER    115    115
SQ   SEQUENCE   115 AA;  12757 MW;  2B1A7C6A9A27C55C CRC64;

  Query Match             58.1%;  Score 496;  DB 1;  Length 115;
  Best Local Similarity   65.5%;  Pred. No. 5.2e-84;
  Matches   78;  Conservative   17;  Mismatches   18;  Indels    6;  Gaps    1;

Qy          1 MESQAQVLISLLLWVSGTCGDIVMTQSPDSLAVSLGERATINCKSSQSLLNSKTRENYLA 60
              ||: |||| |||||:  | |:|||||| ||:|| |||||:|||:|||:        :|||
Db          1 MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSV      --SSYLA 54

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYN 119
              |||||||| |:|||| || | |:|| ||||||||||||||||||: || ||||| | |
Db         55 WYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSN 113


RESULT 14
KVHU_HUMAN
ID   KVHU_HUMAN      STANDARD;      PRT;   113 AA.
AC   P04434;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region VH precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87088282; PubMed=6440122;
RA   Pech M., Zachau H.G.;
RT   "Immunoglobulin genes of different subgroups are interdigitated
RT   within the VK locus.";
RL   Nucleic Acids Res. 12:9229-9236(1984).
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------- ---------- ---------- ---------- ---------- ---------- ----------
DR   EMBL; X02725; -; NOT_ANNOTATED_CDS.
DR   PIR; A01901; KVHUVH.
DR   HSSP; P06326; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    115       IG KAPPA CHAIN V-III REGION VH.
FT   DOMAIN      21     43       FRAMEWORK 1.
FT   DOMAIN      44     54       COMPLEMENTARITY DETERMINING-1.
FT   DOMAIN      55     69       FRAMEWORK 2.
FT   DOMAIN      70     76       COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN      77    108       FRAMEWORK 3.
FT   DOMAIN     109    115       COMPLEMENTARITY DETERMINING 3.
FT   DISULFID    43    108       BY SIMILARITY.
FT   NON_TER    115    115
SQ   SEQUENCE   115 AA;  12757 MW;  51CD55BA53821929 CRC64;

  Query Match             57.6%;  Score 492.5;  DB 1;  Length 115;
  Best Local Similarity   64.2%;  Pred. No. 7.5e-84;
  Matches   77;  Conservative   18;  Mismatches   20;  Indels    5;  Gaps    1;

Qy          1 MESQAQVLISLLLWVSGTCGDIVMTQSPDSLAVSLGERATINCKSSQSLLNSKTRENYLA 60
              |:: |:|| |||||:  | :|||||| |:|| |||||:|||:|||:        :|||
Db          1 MEAPAQLLFLLLLWLPDTTGEIVMTQSPATLSLSPGERATLSCRASQSVSSS      YLA 54

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNL 120
              |||||:| |:|||| || | |:|| ||||||||||||||||||: || ||||| | |
Db         55 WYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW 114
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FT   DOMAIN        21      98        COMPLEMENTARITY DETERMINING 1.
FT   DOMAIN        99      53        FRAMEWORK 2.
FT   DOMAIN        54      60        COMPLEMENTARITY DETERMINING 2.
FT   DOMAIN        61      92        FRAMEWORK 3.
FT   DOMAIN        93     109        COMPLEMENTARITY DETERMINING 3.
FT   DOMAIN       110     119        FRAMEWORK 4.
FT   DISULFID      23      92        BY SIMILARITY.
FT   NON TER      110     110
SQ   SEQUENCE   110 AA;  11950 MW;  60EIA5CB099B1249 CRC64;

  Query Match             57.9%;  Score 364;  DB 1;  Length 110;
  Best Local Similarity   70.5%;  Pred. No. 8.1e-34;
  Matches   79;  Conservative   11;  Mismatches   20;  Indels    2;  Gaps    1;

Qy          21 DIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTR 80
               ||||.|| :|:|:|:|:|||||:|||       :|:|: |||||||||||.|||| ||
Db           1 DIVLTQSPASLAVSLGQRATISCRASQSI   DYH-IHSSMNWYQQKPGQPPKLLIYAASNL 58

Qy          81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCHQSYNLYTFGQGTKVEIK 132
               |||:  :|: |||||||||| |  :: || | |||| |. : : || ||:|||
Db          59 ESGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCHQSEDVWTFGSGTKLEIK 110


Search completed: June 14, 2003, 15:08:47
Job time : 14.94.7 secs
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GenCore version 5.1.6
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M protein - protein search, using sw model

Run on: June 14, 2003, 15:02:49 ; Search time 50.427 Seconds
(without alignments)
539.859 Million cell updates/sec

Title: US-09-249-011B-8
Perfect score: 681
Sequence: 1 MDSQAQVFIFLLLWVSGTCG ..... YCTQSYNLYIIPQSTPKVEIK 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	413.5	60.8	107	11	Q9ER79	Q9er79 mus musculu
2	401	58.9	259	4	Q81CP0	Q81cp0 homo sapien
3	400	58.7	248	11	Q99M37	Q99m37 mus musculu
4	392	57.6	248	11	Q8VC16	Q8vc16 mus musculu
5	389.5	57.2	259	11	Q8VC55	Q8vc55 mus musculu
6	99	57.0	107	4	Q96SA4	Q96sa4 homo sapien
7	384	56.4	107	4	Q9UL81	Q9ul81 homo sapien
8	383.5	56.3	111	11	Q920E9	Q920e9 mus musculu
9	379.5	55.7	108	4	Q9UL77	Q9ul77 homo sapien
10	379	55.7	109	4	Q9UL78	Q9ul78 homo sapien
11	375.5	55.1	108	4	Q9UL79	Q9ul79 homo sapien
12	373.5	54.8	108	4	Q9UL70	Q9ul70 homo sapien
13	372.5	54.7	108	4	Q9UL83	Q9ul83 homo sapien
14	368	54.0	109	4	Q9UL86	Q9ul86 homo sapien
15	368	54.0	109	4	Q9UL85	Q9ul85 homo sapien
16	356.5	52.3	234	11	Q8R062	Q8r062 mus musculu
17	352.5	51.8	124	4	Q9UL87	Q9ul87 homo sapien
18	348.5	51.2	234	11	Q91WE8	Q91we8 mus musculu
19	341	50.1	104	11	Q9JL86	Q9jl86 mus musculu
20	339.5	49.9	233	11	Q91WS9	Q91ws9 mus musculu
21	336.5	49.4	99	11	Q9JI74	Q9ji74 mus musculu
22	333.5	48.8	234	11	Q8VCT6	Q8vct6 mus musculu
23	331.5	48.7	214	11	Q9ECA5	Q9eca5 mus musculu
24	327.5	48.1	108	11	Q8VIJ0	Q8vij0 mus musculu
25	324.5	47.7	103	11	Q9JL80	Q9jl80 mus musculu
26	322	47.3	134	11	Q8VCG3	Q8vcg3 mus musculu
27	319.5	46.9	116	4	Q96PP6	Q96pp6 homo sapien
28	319	46.8	130	4	Q9NP29	Q9np29 homo sapien
29	315.5	46.3	234	11	Q8R028	Q8r028 mus musculu
30	315.5	46.3	298	11	Q9QYF0	Q9qyf0 mus musculu
31	315	46.3	235	11	Q91WL2	Q91wl2 mus musculu
32	309.5	45.4	109	11	Q920E6	Q920e6 mus musculu
33	307.5	45.2	127	11	Q925S9	Q925s9 mus musculu
34	303.5	44.6	101	11	Q9JL78	Q9jl78 mus musculu
35	303.5	44.6	109	6	Q9NSW5	Q9nsw5 oryctolagus
36	300	44.1	241	11	Q921A6	Q921a6 mus musculu
37	296.5	43.5	107	11	Q9JL84	Q9jl84 mus musculu
38	292	42.9	106	5	Q90411	Q90411 schistosoma
39	280.5	41.2	97	11	Q9JL76	Q9jl76 mus musculu
40	267	39.2	237	4	Q8WWX1	Q8wwx1 homo sapien
41	265	38.9	237	4	Q8WTD5	Q8wtd5 homo sapien
42	257.5	37.8	218	11	Q925S1	Q925s1 mus musculu
43	256	37.6	233	4	Q81B09	Q81b09 homo sapien
44	243	35.7	107	4	Q9NSD6	Q9nsd6 homo sapien
45	242.5	35.6	236	4	Q96E61	Q96e61 homo sapien

ALIGNMENTS

RESULT 1
Q9ER79
ID Q9ER79 PRELIMINARY; PRT: 107 AA.
AC Q9ER79;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 17, Last annotation update)
DE Anti human TNF-alpha light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF-a monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single chain antibody gene of a
RT human TNF-alpha specific monoclonal antibody.";
RL Ti 4 Chun i Ta Hsueh Hsueh Pao 1:373-378(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF2[illegible]; AAK53041.1; -.
DR HSSP; P80625; 1WEL.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IG; 1.
DR SMART; SM00409; IGv; 1.
FT NON_TER 1 1 107
SQ SEQUENCE 107 AA; 11784 MW; 2815B1AC0E4A2C7A CRC64;

```
  Query Match             66.4%;  Score 410.5;  DB 11;  Length 167;
  Best Local Similarity   71.0%;  Pred. No. 4.3e-36;
  Matches   76;  Conservative   18;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          24 LDpSfhSIAVSLGEBATISCKASQpSLENSNGKTBLNYLAWYQQKPGQPPKLLIYWASTBESG 83
               :|||| |||:|:|:: |:|||||||:||| |:|||||||:|||| |:|||:|||||||
Db           1 MQpGLhSVAMSVTpGEKVTMSCKSSQ*LVNSGN*pPYTAWYpQKPpQpPKLLVYFASTBESG 60

Qy          84 VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQpSYNL YTFGQGTKV 129
               ||||| |||:|:|||||||||:| ||:| |:| | |   :||| |||:
Db          61 VPDRFMGSGSGTDFTLTISSVQTEDLADYFCQpHYPTPPTFGSGTKL 107


RESULT 2
Q8IT50
ID   Q8IT50      PRELIMINARY;      PRT:   238 AA.
AC   Q8IT50;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 26.2 kDa protein.
OS   Homo Sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LUNG;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022402; AAH22402.1;   -.
KW   Hypothetical protein.
SQ   SEQUENCE   239 AA;  26234 MW;  FACED3A4B038710 CRC64;

  Query Match             58.9%;  Score 401;  DB 4;  Length 239;
  Best Local Similarity   62.8%;  Pred. No. 1.2e-34;
  Matches   81;  Conservative   21;  Mismatches   25;  Indels    2;  Gaps    2;

Qy           5 AQVLTQTTSLSASLGDTVTISCRASQDISNYLNWYQQK 64
               |:|: |:|:| | :: |:|:|||| |: |:|: |:|||:|:|:|: |     || |:||
Db           5 AQTGTGGLMEAVPQGGSLRLSCVVSGFPLSRYGVHWVRQA 63

Qy          65 PDGTVKLLIYWASTRESGVPSRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL YTF 124
               :|||: |:|:: | |:|||||||||||||||||:|:|: |:|||: ||:|: |  ||
Db          64 PPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPFT 123

Qy         125 GQGTKVEIK 133
               |:|||:|||
Db         124 GQGTKLEIK 132


RESULT 3
Q6QM47
ID   Q6QM47      PRELIMINARY;      PRT:   238 AA.
AC   Q6QM47;
DT   01-JUN-2004 (TrEMBLrel. 17, Created)
DT   01-JUN-2004 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2004 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 26.5 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006045; AAH06045.1;   -.
DR   HSSP; P01750; 2FB4.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR003597; Ig_C1_like.
DR   InterPro; IPR003599; Ig_like.
DR   InterPro; IPR003606; Ig_MHC.
KW   Hypothetical protein.
SQ   SEQUENCE   238 AA;  26444 MW;  FB2B06A0B80E330A CRC64;

  Query Match             58.7%;  Score 400;  DB 11;  Length 238;
  Best Local Similarity   62.7%;  Pred. No. 1.6e-34;
  Matches   79;  Conservative   20;  Mismatches   25;  Indels    2;  Gaps    2;

Qy           8 LTLSLSVGDTVTLSCRASQDISNYLNWYQQKPDGTVKLLIYWASTRESGVPSRFSGSGSGTDFT 67
               |:::: |:  :  |:|:|||:| || |||:|:|:|:|||||:|    |: :| |||
Db           7 LLVLMFWIPASSGDVVMTQTPLSLPVSLGDQASISCRSSQSLVHS NGNTYLHWYLQKPG 66

Qy          68 QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL YTFGQG 127
               | |||||  | | |||||||||||||||||:|:|: ||:|||: ||:|: |  |||
Db          67 QSPKLLIYKVSNRFSGVPDRFSGSGSGTDFILKISRVEAEDLGVYYCFQGSHVPYTFGSG 126

Qy         128 TKVEIK 133
               ||:|||
Db         127 TKLEIK 132


RESULT 4
Q8VC16
ID   Q8VC16      PRELIMINARY;      PRT:   238 AA.
AC   Q8VC16;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 26.2 kDa protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019760; AAH19760.1;   -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003606; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS50835; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   238 AA;  26223 MW;  85E5CBE36DE54E6AD CRC64;

  Query Match             57.9%;  Score 394;  DB 11;  Length 238;
  Best Local Similarity   61.9%;  Pred. No. 1.1e-33;
  Matches   78;  Conservative   22;  Mismatches   24;  Indels    2;  Gaps    2;

Qy           6 LTLSLSVGDTVTLSCRASQDISNYLNWYQQKPDGTVKLLIYWASTRESGVPSRFSGSGSGTDFT 65
               |:::: |:  :  |:|:|||:| || |||:|:|:|:|||||:|    |: :| |||
Db           7 LLVLMFWIPASSGDVVMTQTPLSLPVSLGDQASISCRSSQSLVHS NGNTYLHWYLQKPG 66

Qy          66 QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL YTFGQG 125
               | |||||  | | |||||||||||||||||:|:|: ||:|||: ||:|: |  |||
Db          67 QSPKLLIYKVSNRFSGVPDRFSGSGSGTDFILKISRVEAEDLGVYYCFQGSHVPYTFGSG 126

Qy         126 TKVEIK 132
               ||:|||
Db         127 TKLEIK 131
```

RESULT 5
Q8V955
ID Q8V955 PRELIMINARY; PRT; 239 AA.
AC Q8V955;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg E.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC021781; AAH21781.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C1C1190ACA25C337 CRC64;

Query Match 57.2%; Score 389.5; DB 11; Length 239;
Best Local Similarity 64.1%; Pred. No. 2.1e-33;
Matches 82; Conservative 20; Mismatches 24; Indels 4; Gaps 3;

Qy 7 VLLLLLLWVSGTDGDIVLTQSPDSLAVSLGERATINCKSSQSLLNSGNQKNFLTWYQQKPGQPPKLLIYWASTR 66
:::|||| | : |:||||:| || |:|:|:|||||||:|||| || || ||
Db 6 LLVVLLLFTSPAGSNVVLTQSPSILSPVNPGEPVSISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNL 65

Qy 67 PQQPPELLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQDYNL YTFG 124
'|| |:|:|| | || ||||||||||||:|||| || :|||| |||| || || |||
Db 66 PGQSPQLLIYLVSNRFSGVPDRFSGSGSGTDFKLKISRVEAEDVGVYYCFQGNHLPYTFG 125

Qy 125 QGTKVEIK 132
||:|||
Db 126 SGTKLEIK 133

RESULT 6
Q96SA9
ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Anti-streptococcal/cardiac myosin immunoglobulin kappa light chain.
DE Variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98327895; PubMed=9712075;
RA Anderson E.F., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal anti-rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2041(1998).
DR EMBL; U96336; AAB68785.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
FT NON_TER 1 1

FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 49843E9C9B572F1C CRC64;

Query Match 52.8%; Score 360; DB 4; Length 107;
Best Local Similarity 67.9%; Pred. No. 1.1e-33;
Matches 76; Conservative 14; Mismatches 17; Indels 6; Gaps 1;

Qy 21 PPVELQSPDSLAVSLGERATISCKSSQSLLNSGNQKNFLTWYQQKPGQPPKLLIYWASTR 80
|| :|||| || |:|:| |||:|||| :|| |||||||:| |||| ||
Db 1 PSQMEVSTSPSILSAYVGDRVTITCKASQSV- -SYENWYQQKPGKAPNLLIYAASSL 54

Qy 81 EGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQDYNLYTFGQGTKVEIK 132
:|||| |||||||||||||||||||| || | ||| ||| ||| ||:|||
Db 55 QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLITFGQGTKVEIK 106

RESULT 7
Q99L81
ID Q99L81 PRELIMINARY; PRT; 107 AA.
AC Q99L81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277195; PubMed=9614934;
RA Wu X., Lin B., Van der Merwe P.L., Kalis N.N., Bernoy S.M.,
RA Young L.C.;
RT "Myosin reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF077333; AAD56269.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003599; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IGV; 1.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 07054C9FDE0754748 CRC64;

Query Match 56.4%; Score 384; DB 4; Length 107;
Best Local Similarity 66.1%; Pred. No. 2.8e-33;
Matches 74; Conservative 14; Mismatches 19; Indels 6; Gaps 1;

Qy 21 PPVELQSPDSLAVSLGERATISCKSSQSLLNSGNQKNFLAWYQQKPGQPPKLLIYWASTR 80
|| :|||| || |:|:| |||:|||| :|| |||||||:| |||| ||
Db 1 PSQMEVSPSSLSASVGDRVTITCRASQSI- -SNYLNWYQQKPGKAPNLLIYAASSL 54

Qy 81 EGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQDYNLYTFGQGTKVEIK 132
:|||| |||||||||||||||| |||| | ||| ||| ||| ||:|||
Db 55 QSGVPSRFSGSGSGTDFTLTISSLQAEDFAIYYCQQSYSAPIFGQGTKVDIK 106

RESULT 8
Q920E9
ID Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Pteria mimetica kinase anti-idiotype kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 98277139; PubMed 9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Younq D.C.;
RT   "Myosin reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184 192(1998).
DR   EMBL; AF035035; AAD56272.1; -.
DR   HSSP; P01624; 1WEL.
DR   InterPro; IPR003006; Ig MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52E7EE1C7 CRC64;

  Query Match             55.7%;  Score 479;  DB 4;  Length 109;
  Best Local Similarity   68.1%;  Pred. No. 9.8e-44;
  Matches   77;  Conservative   15;  Mismatches   15;  Indels    6;  Gaps    2;

Qy          21 DIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTR 80
               ||||||| |:|:|| |||||:|:::|||| :|     |||||||||||| |:|||| |||
Db           1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSS --   YLAWYQQKPGQAPRLLIYGASSR 56

Qy          81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQ-SYNLYTFGQGTKVEIK 132
               :|:|||||||||||||||||| |: || |||||  |   :  ||| |||||||
Db          56 AIGIPDRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108


RESULT 11
Q90L79
ID   Q90L79      PRELIMINARY;      PRT;   108 AA.
AC   Q90L79;
DT   01-MAY-2000 (TrEMBLrel. 14, Created)
DT   01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 98277139; PubMed 9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Younq D.C.;
RT   "Myosin reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184 192(1998).
DR   EMBL; AF035035; AAD56271.1; -.
DR   HSSP; P01624; 1WEL.
DR   InterPro; IPR003006; Ig MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     108     108
SQ   SEQUENCE   108 AA;  11787 MW;  D8584CE1672418AE CRC64;

  Query Match             55.1%;  Score 475.5;  DB 4;  Length 108;
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```
  Best Local Similarity   67.8%;  Pred. No. 2.3e-32;
  Matches   74;  Conservative   11;  Mismatches   10;  Indels    7;  Gaps    2;

Qy          21 DIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTREENYLAWYQQKPGQPPKLLIYWASTR 80
               ||:|||||  |: | |:| ||||: || :        :|||||||:|:| |:|||| |||
Db           1 DIVMIQSPSSLSASVGDRVTITCPRMS--       -YPYLAWYLQKPRKSPQLLVYAATS 51

Qy          81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNL  YTFGQGTKVEIK 132
               :|||| |||:|||||||||||||||| |||| ||| | ||    ||| |||:|||
Db          52 LASGVPSKFSGSGSGTEFTLTISSLQPDDFATYYCQQYYSYPWTFGQGTKVEIK 107


RESULT 12
Q9ULJ6
ID   Q9ULJ6       PRELIMINARY;       PRT:   108 AA.
AC   Q9ULJ6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035044; AAD56280.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     108     108
SQ   SEQUENCE   108 AA;  11633 MW;  B7BED0E4E4110A37 CRC64;

  Query Match             54.8%;  Score 77.5;  DB 4;  Length 108;
  Best Local Similarity   67.5%;  Pred. No. 3.7e-32;
  Matches   77;  Conservative   11;  Mismatches   17;  Indels    9;  Gaps    3;

Qy          21 DIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTREENYLAWYQQKPGQPPKLLIYWASTR 80
               || :|:|| ||: |:|: ||:|:||| :        |||||||:|||: || ||| |||
Db           1 DIQMTQSPSSLSASVGDRVTITCRASQD--       -NTLAWYQQKPGKVPKLLIYAASTL 54

Qy          81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNL  YTFGQGTKVEIK 132
               :|||| |||||||||||||||||||| |||| ||| | ||    ||| |||:|||
Db          55 QSGVPSKFSGSGSGTDFTLTISSLQPEDVATYYCQQYYSTPWTFGQGTKVEIK 107


RESULT 13
Q9ULJ8
ID   Q9ULJ8       PRELIMINARY;       PRT:   108 AA.
AC   Q9ULJ8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035028; AAD56264.1; -.
DR   HSSP; P01607; 1WIL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     108     108
SQ   SEQUENCE   108 AA;  11628 MW;  2A3325EF2C7DA7B6 CRC64;

  Query Match             54.8%;  Score 77.5;  DB 4;  Length 108;
  Best Local Similarity   67.5%;  Pred. No. 3.7e-32;
  Matches   77;  Conservative   11;  Mismatches   17;  Indels    9;  Gaps    3;

Qy          21 DIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTREENYLAWYQQKPGQPPKLLIYWASTR 80
               || :|:|| ||: |:|: ||:|:||| :        |||||||:|||: || ||| |||
Db           1 DIQMTQSPSSLSASVGDRVTITCRASQD--       -NTLAWYQQKPGKVPKLLIYAASTL 54

Qy          81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNL  YTFGQGTKVEIK 132
               :|||| |||||||||||||||||||| |||| ||| | ||    ||| |||:|||
Db          55 QSGVPSKFSGSGSGTDFTLTISSLQPEDVATYYCQQYYSYPWTFGQGTKVEIK 107


RESULT 14
Q9ULJ6
ID   Q9ULJ6       PRELIMINARY;       PRT:   109 AA.
AC   Q9ULJ6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035028; AAD56264.1; -.
DR   HSSP; P01607; 1WIL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11928 MW;  2A3325EF2C7DA7B6 CRC64;

  Query Match             54.0%;  Score 76.5;  DB 4;  Length 109;
  Best Local Similarity   64.6%;  Pred. No. 1.5e-31;
  Matches   73;  Conservative   18;  Mismatches   16;  Indels    6;  Gaps    2;

Qy          21 DIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTREENYLAWYQQKPGQPPKLLIYWASTR 80
               :|||||||  ||:  |||||:|:|||: :|       ||||:|||||| |:|||| |||
Db           1 EIVLTQSPGTLSLSPGERATLSCRASQSVSS-       YLAWYQQKPGQAPRLLIYGISSR 54

Qy          81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNL  YTFGQGTKVEIK 132
               :|:|:|||||||| ||||||| |: || ||:|: |    ||| |:|:|:|:
Db          55 ATGIPDRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKVDIK 109


RESULT 15
Q9ULB5
```

```
ID   Q_OUIA5       PRELIMINARY;      PRT:   109 AA.
AC   Q_OUIA5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98275154; PubMed=9614941;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernoy S.M.,
RA   Young D.F.;
RT   "Myosin reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF053020; AAC72951.1; -.
DR   HSSP; P01834; 1WEI.
DR   InterPro; IPR003599; Ig_MHC.
DR   InterPro; IPR001596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11761 MW;  FB1E43E7C7AFA07C CRC64;

  Query Match             54.0%;  Score 368;  DB 4;  Length 109;
  Best Local Similarity   66.1%;  Pred. No. 1.5e-41;
  Matches   76;  Conservative   17;  Mismatches   12;  Indels   10;  Gaps    4;

Qy          21 IdVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTR 80
               :||:|||  :|:||  |||||:||  :|||: ::       ||||||||||  |:|||  ||||
Db           1 EIVMTQSPATLSVSPGERATLSCWASQSISSN       LAWYQQKPGQAPRLLIYGASTR 54

Qy          81 GSGVPARFSGSGSGTEFTLTISSLQSEDVAVYYCLQSYNLY   109
               :||  |:|||:|||||||||:|  |:|:| | ||:   |||
Db          55 AIGIPARFSGSGSGTEFTLTISSLQSEDFATYHCQQYNSWPG 108


Search completed: June 11, 2003, 15:12:34
Job time : 46.42 secs
```

GenCore version 5.1.6
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M protein - protein search, using sw model

Run on: June 14, 2003, 15:02:48 ; Search time 48.4194 Seconds
(without alignments)
[illegible] Million cell updates/sec

Title: US-09-249-011b-8
Perfect score: 681
Sequence: 1 MEIVLTQSPATLSLSPGERATLSCRVSES...YSFTGYFMNWVRQAPGQGLEWIGR 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 40847 seqs, 13325023 residues

Total number of hits satisfying chosen parameters: 408470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: [illegible] *
2: [illegible] *
3: [illegible] *
4: [illegible] *
5: [illegible] *
6: [illegible] *
7: [illegible] *
8: [illegible] *
9: [illegible] *
10: [illegible] *
11: [illegible] *
12: [illegible] *
13: [illegible] *
14: [illegible] *
15: [illegible] *
16: [illegible] *
17: [illegible] *
18: [illegible] *
19: [illegible] *
20: [illegible] *
21: [illegible] *
22: [illegible] *
23: [illegible] *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	681	100.0	132	21	AAB07966	A light chain vari
2	629	92.4	132	21	AAB07964	Amino acid sequenc
3	566	83.1	148	13	AAE90078	Light chain of mon
4	564	82.8	289	16	AAK76087	MAb 55.1 light cha
5	580.5	85.2	137	18	AAW10545	Humanised murine a
6	575.5	84.5	137	18	AAW10544	Humanised murine a
7	567.5	83.3	137	21	AAY95243	Humanised antibody
8	559.5	82.2	133	15	AAK59506	Sequence of the li
9	557.5	81.9	133	9	AAP80864	V region of L chai
10	557	81.8	134	18	AAW06206	Xenograft antibody
11	555.5	81.6	240	22	AAU00815	Human immunoglobul
12	555	81.5	141	20	AAY24374	Human monoclonal a
13	554.5	81.4	264	22	ABE43142	Human ovarian anti
14	553.5	81.3	135	21	AAB03714	Immunoglobulin kap
15	548	80.5	241	13	AAR28804	Vector pMR14-7.
16	547.5	80.4	240	20	AAY50141	Human restricted E
17	544.5	80.0	133	17	AAR85004	Monoclonal antibod
18	544.5	80.0	134	20	AAY50690	Human Hum4 VL chai
19	539.5	79.2	133	15	AAK48033	Sequence of Hum4Vl
20	539.5	79.2	134	14	AAK04865	V kappa region of
21	538.5	79.1	137	18	AAW10547	Wild type murine a
22	538.5	79.1	139	17	AAR99469	Monoclonal antibod
23	534.5	78.5	137	18	AAW21655	Chimeric MAb 15-16
24	531.5	78.0	126	21	AAY76734	Amino acid sequenc
25	531.5	78.0	134	18	AAR25158	V region of L chai
26	530.5	77.9	137	18	AAW21654	Mouse MAb 15 light
27	528.5	77.6	133	21	AAY90719	C949 VL region pro
28	528.5	77.6	133	21	AAY57051	Amino acid sequenc
29	528.5	77.6	133	22	AAY02148	Mouse partial anti
30	528.5	77.6	134	14	AAP48317	Sequence encoded b
31	526.5	77.2	133	20	AAY50154	Murine monoclonal
32	526.5	77.2	240	20	AAY50156	Chimeric mouse/hum
33	524.5	77.0	244	21	AAY96395	Human IGBAM 17 immu
34	522.5	76.7	134	22	AAB74702	Anti-CA125 fragment
35	519.5	76.3	154	21	AAB53686	Human colon cancer
36	513.5	75.4	495	19	AAW72486	Growth factor-CAIA
37	513.5	75.4	495	20	AAY06008	CAIAB-IIV antibody
38	507.5	74.5	120	22	AAC85665	Amino acid sequenc
39	505.5	74.2	211	21	ABE43134	Human ovarian anti
40	504.5	74.1	113	20	AAY50145	Antibody F19 human
41	[illegible]	[illegible]	[illegible]	[illegible]	AAB62769	Human B-V 3 mutant
42	[illegible]	[illegible]	[illegible]	[illegible]	AAW42483	Kappa light chain
43	[illegible]	[illegible]	155	20	AAY36012	Human variable kap
44	[illegible]	[illegible]	[illegible]	[illegible]	AAW42482	Creatine kinase MM
45	[illegible]	[illegible]	112	[illegible]	AAY36009	MM amino acid se

ALIGNMENTS

RESULT 1
AAB07966
ID AAB07966 standard; protein; 132 AA.
XX
AC AAB07966;
XX
DT 14-NOV-2000 (first entry)
XX
DE Anti-B7 monoclonal antibody light chain variable region.
XX
KW Antibody 4D1; B7 molecule; B7; humanised immunoglobulin;
KW [illegible] disease; [illegible] disease; inflammatory disorder;
KW [illegible] disease; [illegible] disease; [illegible] problem;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle cell anemia; thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note "signal peptide"
FT Protein 21..132
FT /note "mature protein"
FT Region 44..60
FT /note "complementarity determining region 1"
FT Region 76..82
FT /note "complementarity determining region 2"
FT Region 115..124
FT /note "complementarity determining region 3"

XX
PN WO200047625-A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-GB00463.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524532/47.
DR N-PSDB; AAA59693.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases -
XX
PS Example 1; Fig 1B; 162pp; English.
XX
CC The present sequence represents the light chain variable region of the
CC murine antibody 4D1. The antibody has a binding specificity to B7
CC molecules. The antibody is used to construct humanized immunoglobulins,
CC which comprise an antigen binding region of non-human origin and a
CC portion of a human immunoglobulin. The humanized immunoglobulins are
CC useful for treating autoimmune diseases, infectious diseases,
CC inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 132 AA;

Query Match 92.4%; Score 629; DB 21; Length 132;
Best Local Similarity 90.9%; Pred. No. 1.1e-42;
Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MESQAQVLLFLLLWVSGTCGDIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MESQAQVLLFLLLWVSGTCGDIVLSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLA 60

Qy 61 WYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDVAVYYCQQSYNL 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 WYQQKPGQPPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQQSYNL 120

Qy 121 YTFGQGTKVEIK 132
||||||||||||
Db 121 YTFGQGTKVEIK 132

RESULT 2
AAB07964
ID AAB07964 standard; Protein; 132 AA.
XX
AC AAB07964;
XX
DT 14-NOV-2000 (first entry)
XX
DE Amino acid sequence of light chain variable region of 4D1 antibody.
XX
KW Antibody; 4D1; B7 molecules; B7; humanised immunoglobulin;
KW autoimmune disease; infectious disease; inflammatory disorder;
KW systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "signal peptide"
FT Protein 21..132
FT /note= "mature protein"
FT Region 44..60
FT /note= "complementarity determining region 1"
FT Region 76..82
FT /note= "complementarity determining region 2"
FT Region 115..122
FT /note= "complementarity determining region 3"
XX
PN WO200047625-A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-GB00463.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524532/47.
DR N-PSDB; AAA59693.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases -
XX
PS Example 1; Fig 1B; 162pp; English.
XX
CC The present sequence represents the light chain variable region of the
CC murine antibody 4D1. The antibody has a binding specificity to B7
CC molecules. The antibody is used to construct humanized immunoglobulins,
CC which comprise an antigen binding region of non-human origin and a
CC portion of a human immunoglobulin. The humanized immunoglobulins are
CC useful for treating autoimmune diseases, infectious diseases,
CC inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 132 AA;

Query Match 92.4%; Score 629; DB 21; Length 132;
Best Local Similarity 90.9%; Pred. No. 1.1e-42;
Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MESQAQVLLFLLLWVSGTCGDIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MESQAQVLLFLLLWVSGTCGDIVLSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLA 60

Qy 61 WYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDVAVYYCQQSYNL 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 WYQQKPGQPPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQQSYNL 120

Qy 121 YTFGQGTKVEIK 132
||||||||||||
Db 121 YTFGQGTKVEIK 132

```
LI          1: YIEISSIKLEIK 142


RESULT 4
AAE[illegible]
ID   AAE[illegible] standard; peptide; 148 AA.
XX
AC   AAE[illegible];
XX
DT   14-MAR-1996 (first entry)
XX
DE   Light chain of monoclonal antibody 6A4.
XX
KW   Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.
XX
PN   EP338895-A.
XX
PD   25-OCT-1989.
XX
PF   12-APR-1989;   89EP-0106483.
XX
PR   19-APR-1988;   88DE-3813023.
XX
PA   (BEHR ) BEHRINGWERKE.
XX
PI   Domdey H;  Manser M;  von Specht BU;
XX
DR   WPI; 1989-310861/43.
DR   N-PSDB; AAN91663.
XX
PT   Monoclonal antibody to Pseudomonas aeruginosa  and DNA coding for
PT   variable antibody regions.
XX
PS   Claim 1; page 6; 7pp; german.
XX
CC   The peptide is encoded by the light chain of monoclonal antibody 6A4.
CC   6A4 reacts with the OMP 1 protein of all 19 known serotypes of
CC   P.aeruginosa.  It is used for therapy and diagnosis of infection, and as
CC   a carrier for drugs.  The antibody is IgG2a subclass.
XX
SQ   Sequence   148 AA;

  Query Match             87.5%;  Score 596;  DB 10;  Length 148;
  Best Local Similarity   86.4%;  Pred. No. 4.9e-40;
  Matches  114;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 MDSQVALVLLLLLWVSGTCGSIVLSQSPSILAVSLGERATLSCRASQSLLNSRTRKNYLA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDSQAQVLILLLLWVSGTCGDIVMSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLA 60

Qy         61 WYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNL 120
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WYQQKPKQSPELMVYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCKQSYNL 120

Qy        121 YIEIKR 142
              ||||||
Db        121 YIEIKR 142


RESULT 5
AAE[illegible]
ID   AAE[illegible] standard; Protein; 239 AA.
XX
AC   AAE[illegible];
XX
DT   21-NOV-1995 (first entry)
XX
DE   MAb 55.1 light chain.
XX
KW   Antigen-binding structure; complementarity determining region; CDR;
KW   CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW   monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW   transgenic animal; transgenic plant; antibody engineering;
KW   humanized antibody; immunotoxin.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= sig peptide
FT   Protein         21..239
FT                   /label= Mat protein
FT                   /note= "claim 5, page 98"
XX
PN   WO9515382-A.
XX
PD   08-JUN-1995.
XX
PF   29-NOV-1994;   94WO-GB02610.
XX
PR   03-JUN-1994;   94GB-0011089.
PR   03-DEC-1993;   93GB-0024819.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Blakey DC;  Boot C;  Copley CG;  Hall SM;  Paterson DS;
PI   Rose MS;  Wright AF;
XX
DR   WPI; 1995-210262/28.
DR   N-PSDB; AAQ94056.
XX
PT   Antigen binding structures containing CDRs recognising the CA55.1
PT   antigen - produced by hybridomas and host cells, for use in the
PT   diagnosis and therapy of cancer
XX
PS   Disclosure; Fig.16; 121pp; English.
XX
CC   MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
CC   antigen CA55.1.  cDNAs for the heavy (AAQ94057) and light (AAQ94056)
CC   chains of 55.1 were isolated, and F(ab), F(ab)2, Fab, Fv, scFv or
CC   V-min humanized 55.1 constructs have been expressed in myeloma
CC   cells and E. coli.
XX
SQ   Sequence   239 AA;

  Query Match             86.9%;  Score 592;  DB 16;  Length 239;
  Best Local Similarity   84.8%;  Pred. No. 1.6e-39;
  Matches  112;  Conservative   11;  Mismatches    9;  Indels    9;  Gaps    9;

Qy          1 MDSQVALVLLLLLWVSGTCGSIVLSQSPSILAVSLGERATLSCRASQSLLNSRTRKNYLA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDSQAQVLILLLLWVSGTCGDIVMSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLA 60

Qy         61 WYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNL 120
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WYQQKPKQSPELMVYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCKQSYNL 120

Qy        121 YIEIKR 142
              ||||||
Db        121 YIEIKR 142


RESULT 6
AAW[illegible]
ID   AAW[illegible] standard; Protein; 137 AA.
XX
AC   AAW[illegible];
XX
DT   25-SEP-1997 (first entry)
XX
DE   Humanised murine anti-E-selectin antibody CYT-288V(LB).
XX
KW   Humanised; murine; mouse; E-selectin; antibody; light chain;
KW   variable region; detection; inhibition; mediation; cell adhesion;
KW   diagnosis; reperfusion; inflammation; septic shock; ARDS; sepsis;
KW   acute respiratory distress syndrome; gross cystic breast disease;
```

```
KW   cancer; treatment; splanchnic occlusion shock; psoriasis;
KW   complement; chimeric.
XX
OS   Chimeric - Mus spp.
OS   Chimeric - Homo sapiens.
OS   Synthetic.
XX
PN   W09640942-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US09204.
XX
PR   07-JUN-1995;  95US-0482112.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Bendig MM, Jones ST, Peters C, Saldanha JW, Williams MA;
PI   Jones S;
XX
DR   WPI; 1997-077272/07.
DR   N-PSDB; AAI60729.
XX
PT   Humanised anti E-selectin antibody - useful for diagnosis and
PT   treatment of, e.g. inflammatory responses, septic shock, acute
PT   respiratory distress syndrome or cancer
XX
PS   Claim 17; Page 69; 80pp; English.
XX
CC   The present sequence is the humanised murine anti-E selectin
CC   antibody (Ab) light chain variable region, CY1788V(LA). The Ab can
CC   be used to detect E-selectin, or inhibit E-selectin mediated cell
CC   adhesion. It can also be used to diagnose, reduce or inhibit an
CC   inflammatory response, or the severity of pathologies, e.g. septic
CC   shock, acute respiratory distress syndrome, wound associated
CC   sepsis, gross cystic breast disease or cancer, or treat, e.g.
CC   splanchnic occlusion shock, or psoriasis. It can be administered to
CC   a human without inducing an immune response. In addition, the
CC   effector portion of the Ab can interact with various components of
CC   the human immune system, including complement.
XX
SQ   Sequence  147 AA;

  Query Match             84.5%;  Score 575.5;  DB 18;  Length 147;
  Best Local Similarity   84.2%;  Pred. No. 1.9e-98;
  Matches  112;  Conservative    8;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 MDSQAFVFVSLLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLA 60
              |||| ||||:|| |||||||||||:|||||||||||||||||||:|||||||:|  ||||
Db          5 MESQTQVFMHLLLLWVSGTFGEIVMTQSPESLAVSLGERATINCKSSQSLLHSGNQKNYLT 64

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
              |||||||||||.|||||||||||||||||||||||||||||||||||||||||||||||  |:
Db         65 WYQLKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQNDYSY 124

Qy        121  YTFGQGTKVEIK 132
               |:|:|.|:|||
Db        125 PLTFGAGTKLELK 136


RESULT 6
AAW10944
ID   AAW10944 standard; Protein; 137 AA.
XX
AC   AAW10944;
XX
DT   25-SEP-1997  (first entry)
XX
DE   Humanised murine anti E-selectin antibody CY1788V(LA).
XX
KW   Humanised; murine; mouse; E-selectin; antibody; light chain;
KW   variable region; detection; inhibition; mediation; cell adhesion;
KW   diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
```

```
KW   acute respiratory distress syndrome; gross cystic breast disease;
KW   cancer; treatment; splanchnic occlusion shock; psoriasis;
KW   complement; chimeric.
XX
OS   Chimeric - Mus spp.
OS   Chimeric - Homo sapiens.
OS   Synthetic.
XX
PN   W09640942-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;  96WO-US09204.
XX
PR   07-JUN-1995;  95US-0482112.
XX
PA   (CYTE-) CYTEL CORP.
XX
PI   Bendig MM, Jones ST, Peters C, Saldanha JW, Williams MA;
PI   Jones S;
XX
DR   WPI; 1997-077272/07.
DR   N-PSDB; AAI60729.
XX
PT   Humanised anti E-selectin antibody - useful for diagnosis and
PT   treatment of, e.g. inflammatory responses, septic shock, acute
PT   respiratory distress syndrome or cancer
XX
PS   Claim 17; Page 69; 80pp; English.
XX
CC   The present sequence is the humanised murine anti-E selectin
CC   antibody (Ab) light chain variable region, CY1788V(LA). The Ab can
CC   be used to detect E-selectin, or inhibit E-selectin mediated cell
CC   adhesion. It can also be used to diagnose, reduce or inhibit an
CC   inflammatory response, or the severity of pathologies, e.g. septic
CC   shock, acute respiratory distress syndrome, wound associated
CC   sepsis, gross cystic breast disease or cancer, or treat, e.g.
CC   splanchnic occlusion shock, or psoriasis. It can be administered to
CC   a human without inducing an immune response. In addition, the
CC   effector portion of the Ab can interact with various components of
CC   the human immune system, including complement.
XX
SQ   Sequence  147 AA;

  Query Match             84.5%;  Score 575.5;  DB 18;  Length 147;
  Best Local Similarity   84.2%;  Pred. No. 1.9e-98;
  Matches  112;  Conservative    8;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 MDSQAFVFVSLLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLA 60
              |||| ||||:|| |||||||||||:|||||||||||||||||||:|||||||:|  ||||
Db          5 MESQTQVFMHLLLLWVSGTFGEIVMTQSPESLAVSLGERATINCKSSQSLLHSGNQKNYLT 64

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
              |||||||||||.|||||||||||||||||||||||||||||||||||||||||||||||  |:
Db         65 WYQLKPGQSPQLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQNDYSY 124

Qy        121  YTFGQGTKVEIK 132
               |:|:|.|:|||
Db        125 PLTFGAGTKLELK 136


RESULT 7
AAY95243
ID   AAY95243 standard; Protein; 137 AA.
XX
AC   AAY95243;
XX
DT   29-AUG-2000  (first entry)
XX
DE   Humanised antibody BmOC49 light chain variable region.
XX
KW   Humanised antibody; monoclonal antibody; OC49; BmOC49; CDR;
KW   complementarity determining region; mouse; human; carcinoma;
```

```
KW   colon cancer; tumor associated glycoprotein 72; TAG 72;
KW   tumour marker; diagnosis; therapy.
XX
OS   Chimeric   Mus musculus.
OS   Chimeric   Homo sapiens.
XX
FH   Key                Location/Qualifiers
FT   Region             44..59
FT                      /note= "CDR1"
FT   Region             75..82
FT                      /note= "CDR2"
FT   Region             115..123
FT                      /note= "CDR3"
XX
PN   WO200026394 A1.
XX
PD   11 MAY 2000.
XX
PF   29-OCT-1999;   99WO-US25552.
XX
PR   31-OCT-1998;   98US-0106534.
PR   02-NOV-1998;   98US-0106757.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kashmiri SVS,  Padlan EA,  Schlom J;
XX
DR   WPI; 2000-365637/31.
XX
PT   Chimeric variants of CC49 monoclonal antibodies useful for detecting
PT   and treating cancers associated with the expression of the pancarcinoma
PT   tumor associated antigen TAG-72
XX
PS   Disclosure; Fig 4; 76pp; English.
XX
CC   The present sequence is that of the light chain variable region
CC   (VL) of HuCC49, a humanised monoclonal antibody (MAb) formed by
CC   grafting hypervariable regions from murine MAb CC49 into VL and VH
CC   frameworks of human MAbs LEN and 21/28' CL, respectively, while
CC   retaining murine framework residues required for integrity of the
CC   antigen combining site structure.  HuCC49 binds to the human
CC   pancarcinoma tumor associated glycoprotein-72 (TAG-72), which is
CC   found on the surface of certain human tumours.  The invention is
CC   directed towards mouse-human chimeric variants of CC49 MAbs with
CC   minimal murine content, to methods of making such variants, and
CC   their therapeutic application.  The invention provides
CC   complementarity determining region (CDR) variants of HuCC49 in
CC   which fewer than all 6 CDRs of CC49 are present, and specificity
CC   determining region (SDR) variants of HuCC49 in which only SDRs of
CC   at least 1 CDR from CC49 are present.  Particular variants of HuCC49
CC   have either L-CDR1 and/or L-CDR2 from human MAb LEN.  These
CC   variants have the same or 2 fold lower affinity constant than
CC   HuCC49.  Other variants additionally have corresponding human
CC   residues at position 97 of L-CDR3, and positions 60, 61, 62 and 64
CC   of H-CDR2.  The variants are used in claimed methods of treating
CC   cancer and for detecting cancer cells that express TAG 72.
XX
SQ   Sequence   137 AA;

  Query Match             83.3%;  Score 567.5;  DB 21;  Length 137;
  Best Local Similarity   82.7%;  Pred. No. 8.2e-38;
  Matches  110;  Conservative   11;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 M[illegible]SQAQVLILLLLWV[illegible]IVL[illegible]LAV[illegible]GE[illegible]KRNYLA 60
              |||:|||:||||||||||||||::||||||||||||| |::|||||||| |  ::||||
Db          1 MDSQAQVLMLLLLWV[illegible]IVM[illegible]AV[illegible]EKV[illegible]NYLA 60

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
              ||||:||| |||||||| |||||||||||||||||||||||||:|||||||||| | |:
Db         61 WYQQKP[illegible]KLLIYWASARES[illegible]VAVYY[illegible]YY[illegible] 120

Qy        121  YTFGQGTKVEIK 132
               ||| |||:|:|
```

```
Db        121 PLTFGAGTKLELK 133

RESULT 8
AAR59509
ID   AAR59509 standard; Protein; 133 AA.
XX
AC   AAR59509;
XX
DT   31-DEC-1994  (first entry)
XX
DE   Sequence of the light chain variable region of the mouse NA-8
DE   antibody, including the signal sequence and mature chain.
XX
KW   Antibody NA-8; human CD18; complementarity determining region; CDR;
XX
OS   Mus musculus.
XX
FH   Key                Location/Qualifiers
FT   Protein            21..133
FT                      /label= Mature light chain
XX
PN   WO9412214-A.
XX
PD   09-JUN-1994.
XX
PF   30-NOV-1993;   93WO-US11611.
XX
PR   01-DEC-1992;   92US-0983946.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Co MS,  Landolfi NF;
XX
DR   WPI; 1994-199973/24.
DR   N-PSDB; AAQ66845.
XX
PT   New humanised antibodies specific for CD18 - derived from new
PT   murine antibody NA-8, prevent binding of neutrophils to
PT   endothelial cells, useful for treating inflammation
XX
PS   Disclosure; Fig 1A; 50pp; English.
XX
CC   The mouse antibody NA-8 binds to human CD18. cDNAs for the heavy
CC   chain and light chain variable domain genes of NA-8 were cloned
CC   using anchored PCR. The cDNA variable domain sequences and the
CC   deduced AA sequences are shown in AAQ66845/R59509 and AAQ66846/R59510.
XX
SQ   Sequence   133 AA;

  Query Match             82.2%;  Score 559.5;  DB 15;  Length 133;
  Best Local Similarity   80.5%;  Pred. No. 3.4e-37;
  Matches  107;  Conservative   15;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 M[illegible]SQAQVLILLLLWV[illegible]GDIVLTQS[illegible]LAV[illegible]GERA[illegible]KRNYLA 60
              ||||||||:|||||||||||||||::||| |||||:||: |:||||||||| |  ::||||
Db          1 M[illegible]QA[illegible]VLMLLLLWV[illegible]IVM[illegible]AV[illegible]EKV[illegible]NYLA 60

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
              ||||||| |||||||||||||||||||||:|||||||||||||||::|||:||||| | |:
Db         61 WYQQK[illegible]QSPKLLIYWASTRESGVPDRFT[illegible]TLTISSVKAEDLAVYYCQQYYSY 120

Qy        121  YTFGQGTKVEIK 132
               :||| |||:|||
Db        121 PLTFGSGTKLEIK 133


RESULT 9
AAP80894
ID   AAP80894 standard; protein; 133 AA.
XX
AC   AAP80894;
XX
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```
ID   AAW80498 standard; protein; 134 AA.
XX
AC   AAW80498;
XX
DT   17-FEB-1997 (first entry)
XX
DE   Xenograft antibody BAR 1 kappa light chain variable region.
XX
KW   Xenograft rejection; xenotransplantation; organ transplant;
KW   animal model; hamster; monoclonal antibody; BAR-1.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1..20
FT                   /label= leader
FT   Region          21..43
FT                   /label= FR-1
FT                   /note= "framework region 1"
FT   Region          44..60
FT                   /label= CDR 1
FT                   /note= "complementarity determining region 1"
FT   Region          61..75
FT                   /label= FR-2
FT                   /note= "framework region 2"
FT   Region          76..82
FT                   /label= CDR 2
FT                   /note= "complementarity determining region 2"
FT   Region          83..114
FT                   /label= FR-3
FT                   /note= "framework region 3"
FT   Region          115..122
FT                   /label= CDR-3
FT                   /note= "complementarity determining region 3"
FT   Region          123..134
FT                   /label= FR-4
FT                   /note= "framework region 4"
XX
PN   WO9636658-A1.
XX
PD   21-NOV-1996.
XX
PF   14-MAY-1996;    96WO-US06804.
XX
PR   15-MAY-1995;    95US-0440621.
XX
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI   Cramer DV, Makowka L, Wu G;
XX
DR   WPI; 1997-011852/01.
DR   N-PSDB; AAI43415.
XX
PT   Inhibiting xenograft rejection by modifying antigen expression of
PT   the graft - prevents binding of anti donor antibody and prolongs
PT   graft survival
XX
PS   Claim 11; Page 99; 145pp; English.
XX
CC   A polypeptide (AAW80206) comprises the kappa light chain variable
CC   region of the LEW rat anti-hamster xenograft monoclonal antibody
CC   BAR 1. It is encoded by a cDNA clone (AAI43415) obtd. from a hAR 1
CC   hybridoma light chain cDNA library; the hybridoma was produced by
CC   fusing spleen cells of a LEW rat that had received a hamster heart
CC   transplant, with rat myeloma cells. Recombinant fragments, e.g.
CC   F(ab')2 and Fab', of the antibody block binding of preformed
CC   anti donor xenograft antibodies in a recipient animal serum to
CC   antigen expressed by endothelial cells of the xenograft, i.e. they
CC   inhibit antibody mediated rejection, thereby prolonging the
CC   survival of the hamster xenograft in the recipient.
XX
SQ   Sequence   134 AA;

  Query Match             81.88%;  Score 557;  DB 18;  Length 134;
  Best Local Similarity   78.88%;  Pred. No. 5.4e-87;
  Matches  104;  Conservative   14;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 MESQTQVFVSLLLWVSGTCGDIVLTQSPDSLAVSLGERATINCKSSQSLLNSGTRENYLA 60
              |:|| ||:| ||||||||||||:|||:|| | ||| || :|||||||||| : ::|||
Db          1 MESQIQVLVSMLLWVSGVCGDIVMTQSPDSLAVSVGEKVTMSCKSSQSLLYSGNRKNYLA 60

Qy         61 WYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
              |||||:|||:|||||||||||||||||||||||||||||||||||||||||||||||| | |:  |
Db         61 WYQQKPKQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPRT 120

Qy        121 FGQGTKVEIK 130
              ||||||||||
Db        121 FGAGTKVELK 130


RESULT 10
AAW80206
ID   AAW80206 standard; protein; 134 AA.
XX
AC   AAW80206;
XX
DT   17-FEB-1997 (first entry)
XX
DE   Xenograft antibody BAR 1 kappa light chain variable region.
XX
KW   Xenograft rejection; xenotransplantation; organ transplant;
```

```
                  Score: 1111.5; Pred. No. 1.3e-116; Length 240; 
Qy          1 MWRQKPQLSPKELIYWASIRESGVPSDRFTGSGSGTDFTLTISSVQAEDLAVYYCQQYYNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 MWRQKPQLSPKELIYWASIRESGVPSDRFTGSGSGTDFTLTISSVQAEDLAVYYCQQYYNL 240

Qy        121 YIFGQGTKVEIK 132
              ||||||||||||
Db        241 YIFGAGTKLELK 252


RESULT 11
AAB00815
ID   AAB00815 standard; Protein; 240 AA.
XX
AC   AAB00815;
XX
DT   01-JUN-2001  (first entry)
XX
DE   Human Immunoglobulin superfamily, IgSF, protein #1.
XX
KW   Human; Immunoglobulin superfamily protein; IgSF; Immune response;
KW   inflammatory response; cell-cell interaction; cell-surface recognition;
KW   neural disorder; immune system disorder; muscular disorder;
KW   reproductive disorder; gastrointestinal disorder; pulmonary disorder;
KW   cardiovascular disorder; renal disorder; proliferative disorder;
KW   cancer; common variable adhesion deficiency syndrome; AIDS; SCID;
KW   acquired immunodeficiency syndrome; anaemia; rheumatoid arthritis;
KW   Alzheimer's disease; Crohn's disease; liver cancer; leukaemia;
KW   Hodgkin's lymphoma; Parkinson's disease; Huntington's disease; dementia;
KW   artherosclerosis; stroke; diabetes mellitus; Addison's disease;
KW   urticaria; severe combined immunodeficiency; antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          52..58
FT                   /label= Immunogenic_epitope
FT   Region          68..70
FT                   /label= Immunogenic_epitope
FT   Region          79..90
FT                   /label= Immunogenic_epitope
FT   Region          118..126
FT                   /label= Immunogenic_epitope
FT   Region          146..154
FT                   /label= Immunogenic_epitope
FT   Domain          160..240
FT                   /label= Immunoglobulin_like_domain
FT   Region          183..199
FT                   /label= Immunogenic_epitope
FT   Region          209..215
FT                   /label= Immunogenic_epitope
FT   Region          233..240
FT                   /label= Immunogenic_epitope
XX
PN   WO200181379-A1.
XX
PD   15-MAR-2001.
XX
PF   29-AUG-2000; 2000WO-US23662.
XX
PR   03-SEP-1999;  99US-152248.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (NELS/) NELSEN J.
XX
PI   Young PE, Rosen SM, Shi Y;
XX
DR   WPI; 2001-208084/20.
DR   N-PSDB; AAS00115.
XX
PT   Isolated nucleic acid molecule encoding a human secreted protein is
PT   used in preventing, treating or ameliorating a medical condition -
XX
PS   Claim 11; Page 247; 247pp; English.
XX
CC   The sequence is a Human Immunoglobulin superfamily, IgSF, protein.
CC   a diverse family of proteins involved in cell-cell interactions,
CC   cell-surface recognition, intercellular communication and immune and
CC   inflammatory responses. Polypeptides and antibodies directed to
CC   polypeptides of the present invention are useful to provide immunological
CC   probes for differential identification of tissues. Antibodies can be
CC   used to assay levels of polypeptides encoded by polynucleotides of the
CC   invention. Polypeptides of the present invention can be used to treat
CC   or prevent diseases or conditions such as neural disorders, immune
CC   system disorders, muscular disorders, reproductive disorders,
CC   gastrointestinal disorders, pulmonary disorders, cardiovascular
CC   disorders, renal disorders, proliferative disorders, and/or cancerous
CC   diseases and conditions. Polynucleotides of the invention are also
CC   useful in treating the above disorders. Examples of the disorders
CC   include common variable adhesion deficiency syndrome, acquired
CC   immunodeficiency syndrome (AIDS), anaemia, rheumatoid arthritis,
CC   Alzheimer's disease, Crohn's disease, liver cancer, leukaemia, Hodgkin's
CC   lymphoma, Parkinson's disease, Huntington's disease, dementia,
CC   artherosclerosis, stroke, diabetes mellitus, Addison's disease,
CC   urticaria, severe combined immunodeficiency (SCID). Many more
CC   examples of diseases and disorders are given in the specification.
XX
SQ   Sequence   240 AA;

  Query Match             81.6%;  Score 555.5;  DB 22;  Length 240;
  Best Local Similarity   83.1%;  Pred. No. 1.3e-116;
  Matches  125;  Conservative    9;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 QAQVELLLLWVSGICGALVELQSPPSLAVSLGERATISCKSSQSLLNSGNQKNYLAWYQ 63
              | || | ||||:|| :: |:|||||||||||:|||||||||||:|| |   :|||||||
Db          3 QTQVSLSLLVVSGLCGAVVSMQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQ 62

Qy         64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSVQAEDVAVYYCQQYNL 119
              |||||:|||||||||  |||||:|||||||||||||||||||||||||| | ||  :|
Db         63 QKPGQSPKLLIYWASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLAVYYCQQYYS 118

Qy        120 YIFGQGTKVEIK 132
              ||||||:|||
Db        119 FPGGGTKLEIK 130


RESULT 12
AAY24374
ID   AAY24374 standard; Protein; 141 AA.
XX*
AC   AAY24374;
XX
DT   17-SEP-1999  (first entry)
XX
DE   Human monoclonal antibody against CIGF SEQ ID NO:16.
XX
KW   Human; monoclonal antibody; connective tissue growth factor; CTGF;
KW   cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
KW   skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
KW   rheumatic vascular inflammation.
XX
OS   Homo sapiens.
XX
PN   WO9933870-A1.
XX
PD   08-JUL-1999.
XX
PF   16-DEC-1998;  98WO-JP05697.
XX
PR   16-DEC-1997;  97JP-0346184.
PR   25-DEC-1997;  97JP-0367699.
XX
PA   (NISB-) JAPAN TOBACCO INC.
XX
PI   Sakamoto S, Ishiguro M, Fukatani T, Tomizawa K;
XX
DR   WPI; 1999-413226/36.
DR   N-PSDB; AAX90026.
```

```
XX
PT   New monoclonal antibody reactive with connective tissue growth
PT   factor useful in the treatment of cell proliferation disorders
XX
PS   Claim 16; Page 101-102; 21pp; Japanese.
XX
CC   AAX00026 to AAX00029 encode monoclonal antibodies which react with human
CC   connective tissue growth factor (CTGF). AAY24396 to AAY24398 represent
CC   these monoclonal antibodies. The antibodies are useful in the diagnosis,
CC   prevention and treatment of cell proliferation disorders in which CTGF
CC   is implicated, including fibrosis of lung, kidney, liver and other
CC   tissues; liver cirrhosis; nephritis; skin ulcers and keloid; rheumatoid
CC   arthritis; rheumatic vascular inflammation; hepatitis; and cancer.
XX
SQ   Sequence   142 AA;

  Query Match             81.5%;  Score 555;  DB 20;  Length 141;
  Best Local Similarity   82.4%;  Prod. No. 8.2e-37;
  Matches  108;  Conservative    9;  Mismatches   12;  Indels    2;  Gaps    1;

Qy          4 QAQVLIIIIIWVSGIGGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSGFFEENYLAWYQ 63
              | || | ||||||  |||||||||||||||||||||||||||:|||  |   :|||||||
Db          4 QLQVFISLLIWISAAYGDIVMTQSFQSLAVSLGERATINCKSSQVLYSSNNKNYLAWYQ 63

Qy         64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL--Y 121
              |||||||.|||||||||||||||||||-|||.:|||||||:|||||:|||| | ||:   :
Db         64 QKPGQQPKLLIYWASIRESGVPDRFSGSGSGIDFTLIISSLQAEDVAVYYCQQYYSTPPW 123

Qy        122 TFGQGIKVEIK 132
              |||.|||||:
Db        124 TFGQGTKVEIK 134


RESULT 13
ABP14142
ID   ABP14142 standard; Protein; 264 AA.
XX
AC   ABP14142;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Human ovarian antigen HVVC808, SEQ ID NO:4274.
XX
KW   Human; ovarian antigen; ovary; ovarian tumour; HVVC808; gene therapy;
KW   ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW   infertility; pregnancy disorder; abnormal foetus; polycystic ovary syndrome;
KW   PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW   inflammatory condition; immune disorder; blood disorder;
KW   cardiovascular disorder; respiratory disorder; neurological disorder;
KW   gastrointestinal disorder; urinary system disorder; drug screening;
KW   gene therapy; chromosome mapping; forensic analysis;
KW   antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW   anti-inflammatory; cytotoxic; contraceptive.
XX
OS   Homo sapiens.
XX
PN   WO200224717-A1.
XX
PD   03-JAN-2002.
XX
PF   07-JUN-2001; 2001WO-US018569.
XX
PR   07-JUN-2000; 2000US-0209467P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Birse CE;  Rosen CA;
XX
DR   WPI; 2002-147898/19.
DR   N-PSDB; ABQ56219.
XX
PT   Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT   useful in the prevention, treatment and diagnosis of cancer (e.g.
PT   ovarian cancer), immune disorders, cardiovascular disorders and
PT   neurological diseases
XX
PS   Claim 11; SEQ ID NO 4274; 2922pp; English.
XX
CC   The invention relates to 2179 novel human ovarian antigens (ABP41054-
CC   ABP43228) and 5' cDNAs encoding them (ABQ54181-ABQ56809), and also
CC   encompasses polypeptides 90% identical and polynucleotides 90% identical
CC   to the sequences of the invention. The invention additionally relates to
CC   recombinant vectors and host cells comprising human ovarian antigen
CC   polynucleotides, antibodies against human ovarian antigens, and the use
CC   of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC   treating, prognosing or preventing various ovary and/or breast related
CC   disorders. Such conditions include ovarian cancer and breast cancer, and
CC   metastatic tumours of ovarian or breast origin, reproductive system
CC   disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC   pol, ,zitic  ar, ,ytdrome, ovarian cysts, and dysmenorrhoea), endocrine
CC   disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC   shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC   vaginitis), immune disorders (e.g., congenital and acquired
CC   immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC   blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC   respiratory disorders, neurological disorders, gastrointestinal disorders
CC   and urinary system disorders. Ovarian antigen polypeptides and
CC   polynucleotides may also be used in screening for compounds which
CC   modulate ovarian antigen expression or activity. The polynucleotides may
CC   further be used for gene therapy, chromosome mapping, in the
CC   identification of individuals and in forensic analysis, and the
CC   polypeptides may be used as food additives or to prepare antibodies
CC   useful in disease diagnosis, drug targeting and phenotyping. The present
CC   sequence represents a human ovarian antigen of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   264 AA;

  Query Match             81.4%;  Score 554.5;  DB 23;  Length 264;
  Best Local Similarity   83.1%;  Prod. No. 1.7e-36;
  Matches  108;  Conservative    8;  Mismatches   14;  Indels    2;  Gaps    1;

Qy          4 QAQVLIIIIIWVSGIGGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSGFFEENYLAWYQ 63
              | || | ||||||  |||||||||||||||||||||||||||:|||  |   :|||||||
Db        128 QLQVFISLLIWISAAYGDIVMTQSFQSLAMSLSERATINCKSSQVLYSSNNKNYLAWYQ 187

Qy         64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL--Y 121
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Db        188 QKPGQQPKLLIYWASIRESGVPDRFSGSGSGIDFTLIISSLQAEDVAVYYCQQYYSTPPW 247

Qy        122 TFGQGIKVEIK 132
              |||||||:|||
Db        248 TFGQGTKLEIK 258


RESULT 14
AAB03714
ID   AAB03714 standard; protein; 135 AA.
XX
AC   AAB03714;
XX
DT   04-OCT-2000  (first entry)
XX
DE   Immunoglobulin kappa2 amino acid sequence fragment.
XX
KW   Aortic aneurysm associated antigen protein; AAAP; microtubillar protein;
KW   abdominal aortic aneurysm disease; treatment; detect; tolerance;
KW   immunoglobulin kappa; IgK.
XX
OS   Unidentified.
XX
PN   US6048704-A.
XX
PD   11-APR-2000.
```

```
XX
FF   07-MAR-1997;   97US-0812586.
XX
PR   07-MAR-1996;   96US-0012976.
XX
PA   (UYSY-) UNIV CINCINNATI NEW YORK.
XX
PI   Tilson MD;
XX
DR   WPI; 2000-156667/27.
XX
PT   Isolated micr tibrillar protein for alleviating abdominal aortic
PT   aneurysm disease is purified from human aortic tissue and binds
PT   immunoreactively with immunoglobulin .
XX
PS   Example 3; Column 30; 70pp; English.
XX
CC   The present invention relates to an isolated microfibrillar protein of
CC   approximately 40kD. The protein is isolated from human aortic tissue and
CC   binds immunoreactively with immunoglobulin purified from human abdominal
CC   aortic aneurysm (AAA) tissue. The protein is referred to as aortic
CC   aneurysm-associated antidenic protein (AAAP). The protein is capable of
CC   forming a disulphide bonded dimer. The protein is immunoreactive with
CC   human kappa immunoglobulin. Also included in the invention are
CC   recombinantly produced human AAA proteins. AAAP shows regions of homology
CC   with the bovine microfibril associated glycoprotein MFAP-4 and also with
CC   fibrinogen and vitronectin. The isolated microfibrillar protein is useful
CC   for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
CC   presence of AAA associated immunoglobulin bound to the human aortic
CC   tissue. Antibodies directed against AAAP can be used to detect AAA
CC   disease. The recombinant protein can be used to induce tolerance to
CC   antidenic AAA protein in the subject e.g. human. This sequence represents
CC   an immunoglobulin kappa2 amino acid sequence. The sequence shares
CC   homology with the AAAP of the invention, it was used to identify and
CC   characterise AAAP.
XX
SQ   Sequence  108 AA;

  Query Match          81.4%;  Score 548.5;  DB 21;  Length 145;
  Best Local Similarity   84.6%;  Pred. No. 1e-36;
  Matches  110;  Conservative    5;  Mismatches   14;  Indels    1;  Gaps    1;

Qy           4 QALVLLILLWVSGTCGSIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQ 63
               | || | ||||||||||||||||||||||||||||||||||||||| |   ||||||
Db           4 QPGVPLIPLLWVPGAVGSIVMTQTPLSLAVSLGERATINCKSSQSVLYSSNNRKNYLAWYL 63

Qy          64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPL 122
               |:|:|||||:|||||||||||||||||||||||||||||||||||||| | |:
Db          64 QKPPQQPKLLIYWASTRESGVPDRFIGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPL 123

Qy         123 PGQGTKVEIK 132
               ||||||||||
Db         124 PGQGTKVEIK 133


RESULT 15
AAK28809
ID   AAK28809 standard; Protein; 241 AA.
XX
AC   AAK28809;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Vector pMDR1007.
XX
KW   Plasmid; pMDR1006; pSAB132; vector; pMDR1007, JA221(Iq); Aat II; EcoRV;
KW   pMDR006; BstII; pMDR1003; JA221(Iq); E. coli; ampicillin resistance;
KW   Not I; dephosphorylate; calf alkaline phosphatase; low temperature;
KW   melting agarose; immunoglobulin; kappa chain; signal peptide; LV;
KW   humanised; SAB; light chain; variable region; IV; domain; constant
KW   antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+;
KW   lymphocyte; helper; inducer; HIV; syncytia; formation.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /note= "Immunoglobulin kappa chain signal peptide"
FT   Region          23..134
FT                   /note= "Humanised SAB LV"
FT   Region          135..241
FT                   /note= "Human kappa chain IC"
XX
PN   WO9209705-A.
XX
PD   11-JUN-1992.
XX
PF   27-NOV-1991;   91WO-US008843.
XX
PR   27-NOV-1990;   90US-0618542.
XX
PA   (BIOG-) BIOGEN INC.
XX
PI   Barkley LC;  Chisholm PL;  Kosa JJ;  Kosa MB;  Thomas DW;
XX
DR   WPI; 1992-188609/48.
DR   N-PSDB; AAQ30920.
XX
PT   New anti-CD4 antibody homologues - which bind CD4, do not block
PT   binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT   formation between CD4+ cells
XX
PS   Disclosure; Page 166 7; 205pp; English.
XX
CC   The sequence given is encoded by the insert of the vector pMDR1007.
CC   pMDR1006 (see AAQ30919) and pSAB132 (see AAQ30906) were used in the
CC   construction of this vector. Three fragments were ligated together
CC   to generate pMDR1006; a 572 bp fragment of pMDR985 (see AAQ30914), a
CC   3442bp Aat II/EcoRV fragment of pMDR980 (see AAQ30938) and a 826 bp
CC   EcoRV/BglII fragment of pMDR1004 (see AAQ30990). The ligation mixture
CC   was used to transform E. coli JA221(Iq) to ampicillin resistance.
CC   pMDR1006 was cleaved with Not I and the 5'-3' fragment isolated was
CC   ligated into Not I linearised pSAB132 which had been dephosphorylated
CC   by calf alkaline phosphatase. This generates the plasmid pMDR1007.
CC   The dephosphorylated mixture was fractionated through low temperature
CC   melting agarose and used to transform E. coli JA221(Iq) to ampicillin
CC   resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3'
CC   order, the immunoglobulin kappa chain signal peptide, amino acid (AA)
CC   1-AA112 of the humanised SAB light chain variable region (LV) followed
CC   by synthetic DNA encoding AA1-AA214 of the human kappa light chain,
CC   ie. the light chain constant region (LC). This polypeptide is an
CC   anti-HIV-1 antibody which was shown to bind to CD4 but did not block the
CC   binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+
CC   lymphocytes (helper/inducer cells). The homolog blocked HIV induced
CC   syncytia formation. This homolog can be used in the detection,
CC   prophylaxis and treatment of diseases caused by infective agents whose
CC   primary targets are CD4+ cells.
XX
SQ   Sequence  241 AA;

  Query Match          80.5%;  Score 540;  DB 13;  Length 241;
  Best Local Similarity   83.6%;  Pred. No. 5e-36;
  Matches  107;  Conservative    9;  Mismatches   14;  Indels    2;  Gaps    2;

Qy           5 ALVLLILLWVSGTCGSIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQ 64
               |||| ||||| | ||||||||||||||||||||||||||||||||||||||| |  ||||||
Db           7 AQVLQLGLLWLCGARGSIVMTQTPLSLAVSLGERATINCKSSQSVLYSSNNRKNYLAWYQQ 66

Qy          65 KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLPG 124
               |||||||||||||||||||||||||||||||||||||||||||||| | |:|||||||||
Db          67 KPPQQPKLLIYWASTRESGVPDRFIGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPLPG 126

Qy         125 QGTKVEIK 132
               ||||||||
Db         127 QGTKLEIK 134
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SW protein protein search, using sw model

Run on: June 14, 2003, 15:08:51 ; Search time 17.7928 Seconds
(without alignments)
792.958 Million cell updates/sec

Title: US-09-249-011B-8
Perfect score: 681
Sequence: 1 MDSQAQVLILLLLWVSGICG.....YCIQSYNLVIIGQGIKVEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Prot. No.. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	681	100.0	132	9	US-09-249-011A-8	Sequence 8, Appli
2	627	92.4	239	9	US-09-249-011A-22	Sequence 22, Appl
3	625	92.4	132	9	US-09-249-011A-4	Sequence 4, Appli
4	555.5	81.6	240	10	US-09-799-514-8	Sequence 8, Appli
5	514.5	75.3	154	9	US-09-925-299-1226	Sequence 1226, Ap
6	514.5	75.3	154	10	US-09-925-299-1226	Sequence 1226, Ap
7	504.5	74.1	113	9	US-09-955-529-6	Sequence 6, Appli
8	504.5	74.1	113	9	US-10-121-464-6	Sequence 6, Appli
9	502.5	73.8	113	9	US-09-956-206A-80	Sequence 80, Appl
10	502.5	73.8	113	10	US-09-274-164E-16	Sequence 16, Appl
11	500.5	73.5	113	9	US-10-121-464-2	Sequence 2, Appli
12	498.5	73.2	114	10	US-09-274-164E-2	Sequence 2, Appli
13	498.5	73.2	114	10	US-09-274-164E-6	Sequence 6, Appli
14	497.5	73.1	114	9	US-10-125-687-11	Sequence 11, Appl
15	497.5	73.1	114	10	US-09-274-164E-4	Sequence 4, Appli
16	497.5	73.1	114	12	US-10-025-687-11	Sequence 11, Appl
17	486.5	71.4	114	10	US-09-810-502-88	Sequence 88, Appl
18	485.5	71.4	113	9	US-10-121-464-4	Sequence 4, Appli
19	485.5	71.3	113	9	US-10-144-644-21	Sequence 21, Appl
20	481	70.6	112	9	US-10-056-052-18	Sequence 18, Appl
21	480	70.5	109	10	US-09-828-708-1	Sequence 1, Appli
22	480	70.5	109	10	US-09-828-708-4	Sequence 4, Appli
23	469.5	68.9	127	9	US-09-956-206A-65	Sequence 65, Appl
24	467.5	68.6	153	9	US-09-187-695-62	Sequence 62, Appl
25	460	67.5	130	9	US-10-146-805-7	Sequence 7, Appli
26	459	67.4	101	9	US-10-194-975-89	Sequence 89, Appl
27	459	67.4	101	9	US-10-125-687-25	Sequence 25, Appl
28	459	67.4	101	12	US-10-025-687-25	Sequence 25, Appl
29	456	67.0	112	9	US-10-056-052-10	Sequence 10, Appl
30	457.5	67.2	113	9	US-10-144-644-46	Sequence 46, Appl
31	453.5	66.6	133	9	US-09-874-141-47	Sequence 47, Appl
32	452.5	66.4	113	9	US-10-144-644-45	Sequence 45, Appl
33	451	66.2	112	9	US-10-056-052-6	Sequence 6, Appli
34	450	66.1	112	9	US-10-056-052-14	Sequence 14, Appl
35	449.5	66.0	113	9	US-10-144-644-16	Sequence 16, Appl
36	449	65.9	126	9	US-10-160-232-93	Sequence 93, Appl
37	448.5	65.9	113	9	US-09-995-529-2	Sequence 2, Appli
38	447.5	65.7	239	10	US-09-825-612-9	Sequence 9, Appli
39	446.5	65.6	113	9	US-10-144-644-70	Sequence 70, Appl
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41	445	65.3	113	9	US-09-894-859-2	Sequence 2, Appli
42	445	65.3	113	9	US-09-988-013A-2	Sequence 2, Appli
43	445	65.3	113	10	US-09-741-843-2	Sequence 2, Appli
44	442.5	65.0	220	10	US-09-995-693-1	Sequence 1, Appli
45	440	64.6	235	9	US-10-153-982-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-249-011A-8
; Sequence 8, Application US/09249011A
; GENERAL INFORMATION:
; APPLICANT: [illegible]
; APPLICANT: [illegible]
; APPLICANT: [illegible]
; APPLICANT: [illegible]
; APPLICANT: O'HARA, DENISE
; APPLICANT: KUE, BONITA
; APPLICANT: VELEDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7.2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized
; OTHER INFORMATION: murine anti-human B7.2 light chain
US-09-249-011A-8

Query Match 100.0%; Score 681; DB 9; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.7e-63;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSQAQVLILLLLWVSGICGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSKTRKNYLA 60
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Qy 61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNL 120
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Qy 121 VIIGQGIKVEIK 132
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Db         121 YTFGQGTKVEIK 132


RESULT 2
US-09-249-011A-22
; Sequence 22, Application US/09249011A
; Patent No. US20020165358A1
; GENERAL INFORMATION:
;  APPLICANT: CAO, MAN QING
;  APPLICANT: VASQUEZ, MAXIMILIANO
;  APPLICANT: CARRENO, BEATRIZ
;  APPLICANT: CHELNIKER, ABBIE CHERYL
;  APPLICANT: COLLINS, MARY
;  APPLICANT: GOLDMAN, SAMUEL
;  APPLICANT: GRAY, GARY S.
;  APPLICANT: KNECHT, ANDREA
;  APPLICANT: PAPA, DENISE
;  APPLICANT: POPE, BONITA
;  APPLICANT: VELDMAN, GEERTRUIDA M.
;  TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7.2 AND METHODS
;  TITLE OF INVENTION: OF TREATMENT THEREWITH
;  FILE REFERENCE: 08703.0081-00000
;  CURRENT APPLICATION NUMBER: US/09/249,011A
;  CURRENT FILING DATE: 1999-02-12
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;  LENGTH: 132
;  TYPE: PRT
;  ORGANISM: Mus sp.
US-09-249-011A-22

  Query Match             99.1%;  Score 627;  DB 9;  Length 132;
  Best Local Similarity   99.2%;  Pred. No. 1.6e-42;
  Matches  131;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSKTRENYLA 60
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Db          1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSKTRENYLA 60

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 YTFGQGTKVEIK 132
              ||||||||||||
Db        121 YTFGQGTKVEIK 132


RESULT 3
US-09-249-011A-4
; Sequence 4, Application US/09249011A
; Patent No. US20020165358A1
; GENERAL INFORMATION:
;  APPLICANT: CAO, MAN QING
;  APPLICANT: VASQUEZ, MAXIMILIANO
;  APPLICANT: CARRENO, BEATRIZ
;  APPLICANT: CHELNIKER, ABBIE CHERYL
;  APPLICANT: COLLINS, MARY
;  APPLICANT: GOLDMAN, SAMUEL
;  APPLICANT: GRAY, GARY S.
;  APPLICANT: KNECHT, ANDREA
;  APPLICANT: PAPA, DENISE
;  APPLICANT: POPE, BONITA
;  APPLICANT: VELDMAN, GEERTRUIDA M.
;  TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7.2 AND METHODS
;  TITLE OF INVENTION: OF TREATMENT THEREWITH
;  FILE REFERENCE: 08703.0081-00000
;  CURRENT APPLICATION NUMBER: US/09/249,011A
;  CURRENT FILING DATE: 1999-02-12
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;  LENGTH: 132
;  TYPE: PRT
;  ORGANISM: Murine sp.
;  FEATURE:
;  OTHER INFORMATION: Anti-B7.2 light chain
US-09-249-011A-4

  Query Match             92.4%;  Score 629;  DB 9;  Length 132;
  Best Local Similarity   90.9%;  Pred. No. 2.9e-39;
  Matches  120;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MDSQAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSKTRENYLA 60
              ||||||||||||||||||||||||||||:||| |||||| || |||||||||||||||||||
Db          1 MDSQAQVLILLLLWVSGTKGDIVLSQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPG 60

Qy         61 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNL 120
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WYQQKPGQSPKELIYWASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLAVYYCQQSYNL 120

Qy        121 YTFGQGTKVEIK 132
              |||| ||||||||
Db        121 YTFGGGTKLEIK 132


RESULT 4
US-09-799-514-8
; Sequence 8, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
;  APPLICANT: Young et al.
;  TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and
;  FILE REFERENCE: P1015P1
;  CURRENT APPLICATION NUMBER: US/09/799,514
;  CURRENT FILING DATE: 2001-03-07
;  PRIOR APPLICATION NUMBER: PCT/US99/23662
;  PRIOR FILING DATE: 2000-08-29
;  PRIOR APPLICATION NUMBER: 60/152,248
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;  LENGTH: 240
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-799-514-8

  Query Match             81.6%;  Score 555.5;  DB 10;  Length 240;
  Best Local Similarity   83.1%;  Pred. No. 1.1e-33;
  Matches  108;  Conservative    9;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          4 QAQVLILLLLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLLNSKTRENYLAWYQ 63
              | || | ||||:|| |||:|||||||||||||||||||||||||||| | :||||||
Db          4 QTQVFISLLLWISGAYGEIVMSQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQ 63

Qy         64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLYT 122
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||| : :|
Db         64 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYTSTPYT 123

Qy        123 FGQGTKVEIK 132
              ||||||:|||
Db        124 FGQGTKLEIK 133


RESULT 5
US-09-925-299-1226
; Sequence 1226, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
```

```
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/225,207
;  PRIOR FILING DATE: 2000-08-08
;  PRIOR APPLICATION NUMBER: 60/170,277
;  PRIOR FILING DATE: 1999-12-13
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1225
;  LENGTH: 154
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: SITE
;  LOCATION: (105)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;  NAME/KEY: SITE
;  LOCATION: (131)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;  NAME/KEY: SITE
;  LOCATION: (135)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;  NAME/KEY: SITE
;  LOCATION: (142)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;  NAME/KEY: SITE
;  LOCATION: (145)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;  NAME/KEY: SITE
;  LOCATION: (151)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1225

  Query Match             76.6%;  Score 519.5;  DB 9;  Length 154;
  Best Local Similarity   79.1%;  Pred. No. 3.6e-81;
  Matches  102;  Conservative    7;  Mismatches   19;  Indels    1;  Gaps    1;

Qy           1 QAQVQLVQSGTEVKTPGSSVKVSCKTSGGTFSSYAVSWVRQAPGQGLEWMGGIIPIFGTA 60
               | || | |||||:|| |||||:|||||||||||||||||||||||:| |   :||| |||
Db           6 QTQVFISLLLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLTWYQ 65

Qy          61 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNL-YI 122
               ||||||||||:|||||||||||||||||||||||||||| |||||| ||| | |   :|
Db          66 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISXLQAEDVAVYYCQQYYTIPWT 125

Qy         123 FGQGTKVEI 131
               :|  | |||
Db         126 FGHWTXVEI 134


RESULT 6
US-09-925-299-1225
; Sequence 1225, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/225,207
;  PRIOR FILING DATE: 2000-08-08
;  PRIOR APPLICATION NUMBER: 60/170,277
;  PRIOR FILING DATE: 1999-12-13
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1225
;  LENGTH: 154
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: SITE
;  LOCATION: (105)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;  NAME/KEY: SITE
;  LOCATION: (131)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;  NAME/KEY: SITE
;  LOCATION: (135)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;  NAME/KEY: SITE
;  LOCATION: (142)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;  NAME/KEY: SITE
;  LOCATION: (145)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;  NAME/KEY: SITE
;  LOCATION: (151)
;  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1226

  Query Match             76.6%;  Score 519.5;  DB 9;  Length 154;
  Best Local Similarity   79.1%;  Prod. No. 3.6e-81;
  Matches  102;  Conservative    7;  Mismatches   19;  Indels    1;  Gaps    1;

Qy           1 QAQVQLVQSGTEVKTPGSSVKVSCKTSGGTFSSYAVSWVRQAPGQGLEWMGGIIPIFGTA 60
               | || | |||||:|| |||||:|||||||||||||||||||||||:| |   :||| |||
Db           6 QTQVFISLLLWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLTWYQ 65

Qy          61 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNL-YI 122
               ||||||||||:|||||||||||||||||||||||||||| |||||| ||| | |   :|
Db          66 QKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISXLQAEDVAVYYCQQYYTIPWT 125

Qy         123 FGQGTKVEI 131
               :|  | |||
Db         126 FGHWTXVEI 134


RESULT 7
US-09-995-529-6
; Sequence 6, Application US/09995529
; Publication No. US20030099659A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT: Huse, William D.
;  APPLICANT: Tang, Ying
;  TITLE OF INVENTION: Humanized Collagen Antibodies and
;  TITLE OF INVENTION: Related Methods
;  FILE REFERENCE: P IX 4976
;  CURRENT APPLICATION NUMBER: US/09/995,529
;  CURRENT FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;  LENGTH: 115
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-995-529-6

  Query Match             74.1%;  Score 504.5;  DB 9;  Length 115;
  Best Local Similarity   86.7%;  Prod. No. 4.1e-80;
  Matches   98;  Conservative    7;  Mismatches    7;  Indels    1;  Gaps    1;

Qy           2 VQLVQSGTEVKTPGSSVKVSCKTSGGTFSSYAVSWVRQAPGQGLEWMGGIIPIFGTANY 61
               |||||||||||||||||||||||||||||| |   :|||||||||||||||||||||||||
Db           1 VQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60

Qy          62 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGSYYYDFWSGYPLEYWGQGTLV 121
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGSYYYDFWSGYPLEYWGQGTLV 120

Qy         122 TVSS 125
               ||||
Db         121 TVSS 124


RESULT 8
US-10-121-464-6
```

; Sequence 2, Application US/10121464
; Publication No. US2003010996A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: Boehringer Ingelheim Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer treatment by using FAP alpha specific antibodies
; FILE REFERENCE: 1 120411
; CURRENT APPLICATION NUMBER: US/10/121,464
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/284,868
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antibody
; OTHER INFORMATION: Sequence
US-10-121-464-2

Query Match 73.8%; Score 502.5; DB 9; Length 113;
Best Local Similarity 87.6%; Pred. No. 4.3e-30;
Matches 99; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 21 DIVLTQSPDSLAVSLGERATINCKSSQSLLNSGTTPENYLAWYQQKPGQPPKLLIYWASTR 80
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSLLYSPNQKNYLAWYQQKPGQPPKLLIYWASTR 60

Qy 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLYTFGQGTKVEIK 132
Db 61 ESGVPDRFSGSGSGTDFILTISSLQAEDVAVYYCQQYFSYPLTFGQGTKVEIK 113

RESULT 9
US-09-956-206A-80
; Sequence 80, Application US/09956206A
; Patent No. US20020164599A1
; GENERAL INFORMATION:
; APPLICANT: G. P[illegible], FERNANDO J.E.
; APPLICANT, ROBERTO L.
; APPLICANT, DEBBY A.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES DERIVED FROM THE
; MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY EFFICIES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Pa[illegible] Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,206A
; FILING DATE: 19-Apr-2002
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/[illegible]
; FILING DATE: 11-SEP-1995
; APPLICATION NUMBER: PCT/US97/[illegible]
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: 08/487,[illegible]
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/[illegible]
; FILING DATE: 16-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEIL, ERIC
; REGISTRATION NUMBER: 44,408
; REFERENCE/DOCKET NUMBER: 27633/20001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-956-206A-80

Query Match 73.8%; Score 502.5; DB 9; Length 113;
Best Local Similarity 87.6%; Pred. No. 4.3e-30;
Matches 99; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 21 DIVLTQSPDSLAVSLGERATINCKSSQSLLNSGTTPENYLAWYQQKPGQPPKLLIYWASTR 80
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSLLYSPNQKNYLAWYQQKPGQPPKLLIYWASTR 60

Qy 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLYTFGQGTKVEIK 132
Db 61 ESGVPDRFSGSGSGTDFILTISSLQAEDVAVYYCQQYFSYPLTFGQGTKVEIK 113

RESULT 10
US-09-274-163E-16
; Sequence 16, Application US/09274163E
; Patent No. US20020137897A1
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: WILKINS STEVENS, Priscilla
; APPLICANT: RAFFEN, Rosemarie
; APPLICANT: SCHIFFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 05193-0224
; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 09/274,380
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-274-163E-16

Query Match 73.8%; Score 502.5; DB 10; Length 113;
Best Local Similarity 86.7%; Pred. No. 4.3e-30;
Matches 98; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 21 DIVLTQSPDSLAVSLGERATINCKSSQSLLNSGTTPENYLAWYQQKPGQPPKLLIYWASTR 80
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60

Qy 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLYTFGQGTKLEIK 132
Db 61 ESGVPDRFSGSGSGTDFILTISSLQAEDVAVYYCQQYYSTPYSFGQGTKLEIK 113

RESULT 11
US-10-121-464-2
; Sequence 2, Application US/10121464
; Publication No. US2003010996A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: Boehringer Ingelheim Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer treatment by using FAP alpha specific antibodies

; FILE REFERENCE: I 125611
; CURRENT APPLICATION NUMBER: US/10/125,494
; CURRENT FILING DATE: 2002 11 15
; PRIOR APPLICATION NUMBER: [illegible]
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antibody
; OTHER INFORMATION: Sequence
US-10-125-494-2

Query Match 73.7%; Score 500.5; DB 9; Length 114;
Best Local Similarity 88.0%; Pred. No. 6e-30;
Matches 101; Conservative 5; Mismatches 5; Indels 4; Gaps 2;

Qy 21 DIVLTQSPDSLAVSLGERATISCKSSQSLLNSRTRENYLAWYQQKPGQPPKLLIYWASTR 80
DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRENYLAWYQQKPGQPPKLLIYWASTR 60

Qy 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYNLTFGQGTKVEIK 132
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPFTFGQGTKLEIK 114

RESULT 13
US-09-274-163E-2
; Sequence 2, Application US/09274163E
; Patent No. US20020137867A1
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: WILKINS STEVENS, Priscilla
; APPLICANT: RAFFEN, Rosemarie
; APPLICANT: SCHIFFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 05584/0224
; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 08/374,480
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-274-163E-2

Query Match 73.2%; Score 499.5; DB 10; Length 114;
Best Local Similarity 85.8%; Pred. No. 8.5e-30;
Matches 97; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

Qy 21 DIVLQSPDSLAVSLGERATINCKSSQSLLNSRTRENYLAWYQQKPGQPPKLLIYWASTR 80
DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASIR 60

Qy 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPFTFGQGTKVEIK 132
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYSFPYSFGQGTKLEIK 114

RESULT 14
US-10-125-687-11
; Sequence 11, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Inc, Dyax
; TITLE OF INVENTION: STRUCTURE BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 20050.705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody light chain variable region
US-10-125-687-11

Query Match 73.1%; Score 497.5; DB 9; Length 114;
Best Local Similarity 86.7%; Pred. No. 1e-29;
Matches 98; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

Qy 21 DIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRENYLAWYQQKPGQPPKLLIYWASTR 80
DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASIR 60

Qy 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYNLTFGQGTKVEIK 132
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPFTFGQGTKLEIK 114

RESULT 15
US-09-274-163E-4
; Sequence 4, Application US/09274163E
; Patent No. US20020137867A1
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: WILKINS STEVENS, Priscilla
; APPLICANT: RAFFEN, Rosemarie
; APPLICANT: SCHIFFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 05584/0224
; CURRENT APPLICATION NUMBER: US/09/274,163E

; APPLICANT: SCHIFFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 05584/0224
; CURRENT APPLICATION NUMBER: US/09/274,163E
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 08/374,480
; PRIOR FILING DATE: 1995-01-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-274-163E-6

Query Match 73.2%; Score 498.5; DB 10; Length 114;
Best Local Similarity 87.0%; Pred. No. 8.5e-30;
Matches 97; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

Qy 21 DIVLQSPDSLAVSLGERATINCKSSQSLLNSRTRENYLAWYQQKPGQPPKLLIYWASTR 80
DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASIR 60

Qy 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYNLTFGQGTKVEIK 132
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPFTFGQGTKLEIK 114

RESULT 14
US-10-125-687-11
; Sequence 11, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Inc, Dyax
; TITLE OF INVENTION: STRUCTURE BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 20050.705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody light chain variable region
US-10-125-687-11

Query Match 73.1%; Score 497.5; DB 9; Length 114;
Best Local Similarity 86.7%; Pred. No. 1e-29;
Matches 98; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

Qy 21 DIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRENYLAWYQQKPGQPPKLLIYWASTR 80
DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASIR 60

Qy 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYNLTFGQGTKVEIK 132
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSYPFTFGQGTKLEIK 114

RESULT 15
US-09-274-163E-4
; Sequence 4, Application US/09274163E
; Patent No. US20020137867A1
; GENERAL INFORMATION:
; APPLICANT: STEVENS, Fred J.
; APPLICANT: WILKINS STEVENS, Priscilla
; APPLICANT: RAFFEN, Rosemarie
; APPLICANT: SCHIFFER, Marianne
; TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
; FILE REFERENCE: 05584/0224
; CURRENT APPLICATION NUMBER: US/09/274,163E

; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: US 08/474,884
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-249-011B-4

Query Match 76.1%; Score 467.5; DB 10; Length 114;
Best Local Similarity 85.8%; Pred. No. 1e-29;
Matches 97; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

Qy 21 DIVLTQSPASLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTR 80
DIVLTQSPASLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQPPKLLIYWASTR
Db 1 DIVMTQSPSSLAVSVGEKVTMSCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASTR 60

Qy 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYNLYTFGQGTKVEIK 132
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYSTPYSFGQGTKLEIK 114

Search completed: June 14, 2003, 15:15:19
Job time : 18.7978 secs